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APEC-ATCWG Workshop on

Capacity Building for Development and Implementation of Risk Management Systems on Genetic Resources

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Proceedings of the APEC-ATCWG Workshop on

Capacity Building for Development and Implementation of Risk Management Systems on Genetic Resources

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Preface

The APEC-ATCWG International Workshop, “Capacity Building for Development and Implementation of Risk Management Systems on Genetic Resources for Food and Agriculture”, was held at the Taiwan Agricultural Research Institute (TARI), Council of Agriculture, Chinese Taipei, on 14~17 October, 2008.

Genetic resources are the basis to not only the conventional breeding for improving crop yield and quality, but also the innovated biotechnology in utilizing crop traits for further improvement. However, there is a potential risk of losses of genetic resources due to factors such as human incautiousness, nature disaster, and climate change. As food supply remains an important global issue, it is so crucial to find effective measures for the improvement of risk management and conservation of genetic resources.

The objective of the APEC-ATCWG Workshop is to share experiences and knowledge on risk management of germplasms among APEC member economies. Through the multilateral communication and discussion on risk management of genetic resources at this workshop, I believe all member economies could actively promote further cooperation to ensure effective conservation and efficient utilization of all genetic resources. In addition, the workshop would also benefit all member economies by improving food supply, agricultural product, and social prosperity as well.

A total of 32 participants from 12 member economies attended the workshop, including six invited resource speakers and representatives. The Workshop consisted of plenary sessions, major symposia (including resource presentations and country reports), and field tours to visit scientific institutions, project areas, etc. In the symposium, Dr. Jessica Kathle, Director of NordGen addressed the experiences and practical measures for establishing an international seed bank “Svalbard Global Seed Vault” which is the most secure possible backup storage site for a global system of *ex situ* collections of crop diversity. The proceedings containing expert papers as well as country reports presented in the workshop would be useful and valuable to risk management to the APEC member economies.

I would like to express my sincerest appreciation to all participants for their attendance and valuable contributions in this workshop. The publication of the proceedings would not have been possible without the financial support from the Council of Agricultural and the excellent assistance of the staff of TARI.

Dah-Jiang Liu, Ph.D.

Director General
Taiwan Agricultural Research Institute
Council of Agriculture, Chinese Taipei

Opening Remarks

Dr. Wu-Hsiung Chen
Minister
Council of Agriculture, Chinese Taipei

Director General Liu**,** Honorable Participants, Ladies and Gentlemen:

On behalf of the host economy Chinese Taipei, I would like to welcome all of you to this meaningful activity of APEC, namely the “2008 APEC-ATCWG International Workshop on Capacity Building for Development and Implementation of Risk Management Systems on Genetic Resources for Food and Agriculture”, held here at the Taiwan Agricultural Research Institute. Dr. Liu and his capable staff have worked hard to ensure a good start for this important workshop.

As we all know, agriculture is crucial to economic development and social stability in the APEC economies. Recently, with the soaring food prices which have led to social and economic disruptions in parts of the world, people around the world once more realize how important agriculture is in their economies.

In order to ensure adequate food supply to all human beings, improvement in food production by traditional or biotechnological methods is happening almost every minute and everywhere in the world. But the improvement has to depend upon the full utilization of genetic resources and the effective application of research findings. Genetic resources have been recognized worldwide as essential assets for food and agricultural development, and they exert strong impacts on the global economy, social welfare, and the environment.

In the past few decades, rapid economic growth in many APEC economies may have resulted in losses of genetic resources of plants and wildlife. Therefore, risk management is a key strategy to reduce or prevent potential losses of genetic diversity so as to ensure sustainable development in the food and agricultural sector. The strategy should include the development of technologies for the management of all genetic resources and the application of these technologies in preventing further losses of genetic resources caused by human activities or natural disasters. Therefore, we can say that the preservation of genetic resources also serves as the basis for agricultural development. The establishment of the

Arctic Noah's Ark plant kingdom in Norway provides a significant example of public awareness of the urgent need for worldwide preservation of genetic resources.

In the realm of genetic resources preservation, there are lots of experience and expertise which could be shared among APEC economies. Chinese Taipei is greatly honored to host a workshop dedicated to this cause. Through the sharing of research findings of the experts and the exchange of experience and expertise among the participants, I think we are confident that this workshop will proves a great aid in helping APEC economies to formulate effective risk management systems on genetic resources for food and agriculture.

It is my hope that all the participants of this workshop will utilize this valuable opportunity to deliberate not only on the core issues but also on related issues and problems faced in the vast domain of genetic resources preservation. I believe through your active participation and contribution on this workshop will be of help to future sustainable development in agriculture.

In addition to the workshop itself, we have arranged field trips to the Livestock Research Institute, the Fisheries Research Institute, the World Vegetable Center, the Food Industry Research and Development Institute, a recreational farm, and the National Palace Museum. We hope the tour will enable all participants from abroad to know more about Taiwan’s animal, vegetable, freshwater fish, and microorganism genebanks and its cultural heritage.

Before concluding my remarks, I wish all the participants a rewarding experience and the workshop a great success.

Thank you for your attention.

Welcome Remarks

Dr. Dah-Jiang Liu
Director General
Taiwan Agricultural Research Institute
Council of Agriculture, Chinese Taipei

Mr. Minister of the Council of Agriculture of Chinese Taipei, Dr. Keating, Director General of the World Vegetable Center; Dr. Kathle, Director of the Nordic Genetic Resource Center from Sweden, Distinguished Speakers, Dear Participants, Ladies and Gentlemen:

On behalf of the Taiwan Agricultural Research Institute, I sincerely welcome all of you attending the "2008 APEC Workshop on the Risk Management Systems on Genetic Resources", especially those international friends coming all the way to Taiwan.

The importance of genetic resources has long been recognized as valuable treasures for human beings. It is important not only to global economy through facilitating food and agricultural production, but also to the sustained development of human culture and welfare by its impacts on the environment. Back in 1997, with the support from the APEC authorities, Chinese Taipei initiated and held the first workshop on agricultural genetic resources here in this Institute. Five more workshops have been held in different Member Economies during the past 10 years. We are happy to see that the mainstream still keeps moving strong. And today, we are here again to move one step forward to the seventh Workshop.

Our past experiences have taught us more than enough lessons that there are always high risks of losing genetic resources under various occasions. Any plant or animal species, once being extinct, can never be recovered. On the other hand, it's negative or harmful influence on the environment and human beings lasts endlessly. This is why risk management is so critical to germplasm conservation. This is also why we are here today trying to equip ourselves better in order to save more genetic resources which mean so much to us and to the earth we live on.

We believe that minimizing the risk can be achieved if we utilize and maintain properly the precious genetic resources. Improving the strategies of risk management will be targeted in many presentation and discussion sections of this Workshop. I am confident that all the experts and representatives from APEC Member Economies could benefit by attending this

very meaningful Workshop. However, may be we can do a little bit more beyond the workshops we have held for seven times. For example, holding training courses for and facilitating the exchange of agricultural germplasm among APEC Member Economies might be issues worth to be considered. Should such issues be raised and approved by the participants of this Workshop, I would like to report it to Mr. Minister of COA for his consent and possible materialization in the near future.

Finally, I would like to express my appreciation to Mr. Sheng-Chung Huang, Director of the Plant Germplasm Division, and my colleagues of this Institute for their hard working and thoughtful arrangement of the Workshop. My best wishes to all the participants and observers. I wish that in addition to risk management of genetic resources, you have warm friendship and happy memories packed in your hearts when you go back home a few days later. To our foreign friends, please enjoy your stay in Taiwan to the utmost you can. Believe me, this is a very beautiful, lovely and friendly country.

Thank you.

Congratulatory Remarks

Dr. Dyno Keatinge
Director General
AVRDC – The World Vegetable Center
Shanhua, Tainan, Taiwan

Your Excellency Mr. Chen, Director General Dr. Liu,

I would like to say first of all that I heartily congratulate the Government of the Republic of China for taking on board this particular workshop. I would like to pick out one word that I believe to be the most important for this workshop and that is the word: risk. I believe that we are entrusted with genetic resources not just for today but for many generations in the future, and it is amazing when we consider the seriousness of the responsibility we undertake with that promise to our great, great, great grand children. I believe that to be the most risky thing we need to consider when we are here today.

When we take on the responsibility for germplasm on behalf of FAO, it is in perpetuity. Now that is a very scary word in English, which could mean forever, ever and ever. Now I can see my budget for this year and perhaps next but I can't see much beyond that. But nevertheless it is something that we have to tackle but I believe it is necessary for us to tackle it together and that is why it is important that the international community in this particular case, APEC, have gathered us together today because I don't believe the responsibility lies with one institution, one government or whatever. It is the responsibility for all of us here globally and we need to maximize our collaboration in order to do so.

Many people who are new to Taiwan are not aware that it there is a very long history of agriculture research here and I congratulate this nation for doing that. I think in the UK as early as in 1870s Rothamsted Agricultural Research Institute was founded, the first in the world perhaps, but not much earlier than here in Taiwan in 1895. This nation has been involved in strategic research for a very long period. I believe that is one of the reasons why when we had the recent food crisis here, people could say rice price crisis in Taiwan because food insecurity has never been a common problem in this particular beautiful island.

At least before that time the Government has set their policy over the years of allowing their agriculture institutions to keep pace with industrial development and they have not sacrificed their agriculture industry as so many other countries have over the last few years. Because of that when the food crisis came, then they had adequate spare capacity to deal with it.

I do recognize that as agriculture becomes of higher and higher importance and is intensifying itself more and more there is a tendency towards the erosion of species, the erosion of germplasm. Nevertheless I believe that there is now a recognition that crop diversification is important. This is a dimension of agriculture which the World Vegetable Center currently believes in and that we presently represent, I believe, one of the leading edges of research in that area.

But if you look around in Taiwanese agriculture you can see hundred and hundred of species have successfully been employed in the agriculture sector from dragon fruit, rice, different vegetables, and livestock etc. There is a broader base for agriculture here which I believe to be an important conclusion which perhaps probably countries in the EU, like the UK, might learn from as they have been eroding their agriculture base for many years now.

So I would like to congratulate again the Government of this country for setting us all an excellent example on how to maintain and use their genetic resources, how to maintain and develop their agricultural industry, how to maintain and develop their agriculture research, and I believe that is very important too in long term and I would ask you all to join me in another round of applause for Taiwan so that they can continue to behave as an excellent example to the whole world.

Thank you very much.

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Capacity Building for Risk Management Systems on Genetic Resources
1~20

Experiences from Establishing an International Seed Bank – Svalbard Global Seed Vault – Practical Management Measures

Jessica Kathle[1]

NordGen and Martin Cleemann Rasmussen, Advisor, NordGen

Abstract

The experiences and practical measures from establishing an international seed bank – Svalbard Global Seed Vault (SGSV) – are described in this paper. Build to serve as the most secure safety backup storage site for seeds on food crops conserved by seed banks worldwide and for a global system of *ex situ* collections of crop diversity, the paper presents the background for establishing the SGSV, its vision and framework, the structure and organization, the depositor agreement and the present day status of the SGSV.

Introduction of NordGen

The Nordic Genetic Resource Center (NordGen) was established by the Nordic Ministries on the first of January 2008 by merging the Nordic Gene Bank (NGB), the Nordic Gene Bank for Farm Animal (NGH) and the Nordic Council of Forest Reproductive Material (NSFP). The new institution is based upon more than 30 years of successful cooperation within genetic resources between the 5 Nordic countries; Norway, Sweden, Finland, Denmark, and Island. NordGen's main office is in Sweden (Alnarp), where the Nordic gene bank for seeds is also located, while the departments of farm animal and forest trees are in Norway. In addition there are networks and focal persons in all of the Nordic countries. The activities of NordGen cover conservation and sustainable use of genetic resources within crops, farm animal and forest trees. NordGen has a strong engagement both in influencing the international regulations and framework of genetic resources, and in assisting in the building and the managing of gene banks in developing countries. The mandate of NordGen has

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recently been expanded to include environmental issues linked to genetic resources relevant for food and agriculture which underlines our interdisciplinary approach.

Background for Svalbard Global Seed Vault

The history of what is today known as the Svalbard Global Seed Vault (SGSV) starts in 1984, when NordGen (at that time the Nordic Gene Bank) established its safety storage for its Nordic collections of seed on Svalbard in the permafrost of the closed down mine in the vicinity of the Svalbard capital Longyearbyen.

The positive experience of the storage by NordGen in the permafrost at Svalbard quickly led to the question of a safety deposit of seeds for the whole world being taken up by scientists and by the UN's Food and Agriculture Organization and the International Board for Plant Genetic Resources (IBPGR). Unfortunately a lack of funding and the lack of international frameworks and rules for the exchange of seeds between countries severely hampered the process. The necessary frameworks came in place when the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) came into force in 2004 which regulated the exchange of crop material. A real breakthrough appeared at the end of 2004, when an expert group strongly recommended the establishment of safety storage of seeds from the whole world at Svalbard and presented this to the FAO's Commission for Genetic Resources for Food and Agriculture. The report pointed to the important combination of Svalbard's geographical location, the very positive storage experiences since 1984 and the fact that several developing countries could already point to the very positive collaboration with the Nordic countries and NordGen. The group also pointed out, that Svalbard fulfilled even the worst case security requirements for long term storage. The recommendations of the report received the support of FAO's Commission for Genetic Resources for Food and Agriculture and in the autumn of 2005 a steering group led by the Norwegian Ministry for Food and Agriculture and consisting of the Global Crop Diversity Trust (GCDT), NordGen, CGIAR and others commenced the planning for world seed storage at Svalbard. In May 2007 the construction of the facility was commenced and in February 2008, the Svalbard Global Seed Vault (SGSV) was officially opened to the world.

The vision and the framework

The tasks and challenges facing the genetic resources and the gene banks of the world today are many. War, natural disasters, climate change and a lack of adequate funding all constitute severe risks for the gene banks and the material stored in these. The SGSV plays a crucial role in meeting these tasks and challenges, and this is reflected in the vision of the SGSV, which states that:

- the Svalbard Global Seed Vault will provide a global security net;
- the Svalbard Global Seed Vault shall be the securest possible backup storage site for a global system of ex situ collections of crop diversity; and
- Svalbard Global Seed Vault shall have the capacity to conserve all unique plant genetic diversity relevant for food and agriculture held in conventional seed banks around the world.

To achieve this, the SGSV is run in accordance with the international framework – The Convention on Biological Diversity (CBD) and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA). The SGSV therefore has the same objectives i.e. the conservation and sustainable use of biodiversity and a fair and equitable sharing of the benefits derived from their use.

The structure of the SGSV

The actual structure of the SGSV is designed to meet all the requirements for long-term storage with maximum security. The capacity of the vault is twice the amount of all known seeds stored in the gene banks of today. The facility is located at a geologically stable location 130 meters above sea level (above even the worst climate change scenario), the three storage halls are embedded 120 meters into the mountainside in solid rock, the temperature is maintained at a constant –18°C and permafrost works as a natural freeze guarantee at –4°C in the event of equipment failure (Fig. 1 and 2). The facility is further secured through a number of monitoring and surveillance with gas-, temperature- and motion-detectors. The many polar bears roaming the area of Svalbard provide yet another – though less controllable security for the facility!

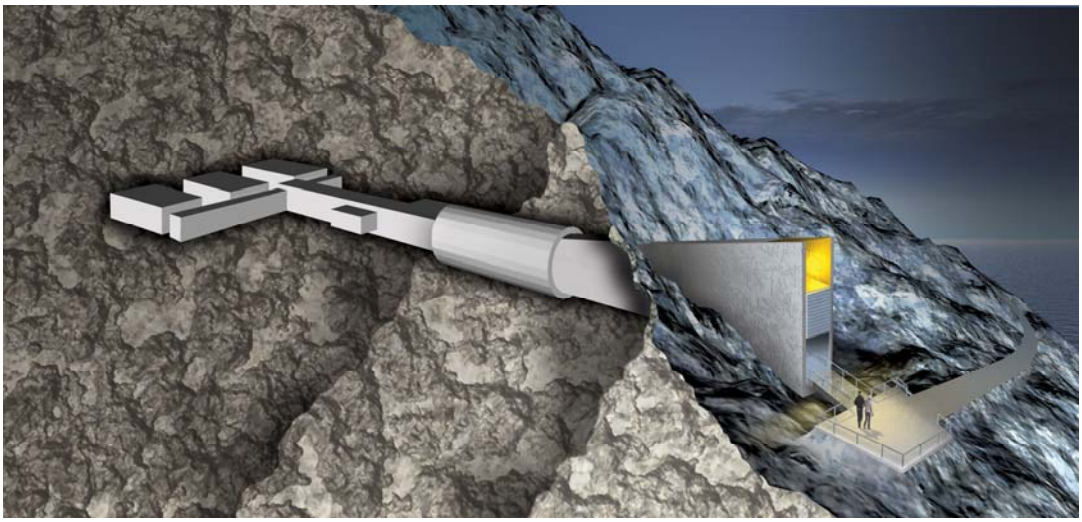

Fig. 1. The entrance of SGSV and a cross-section of the seed vault deep inside the mountain.

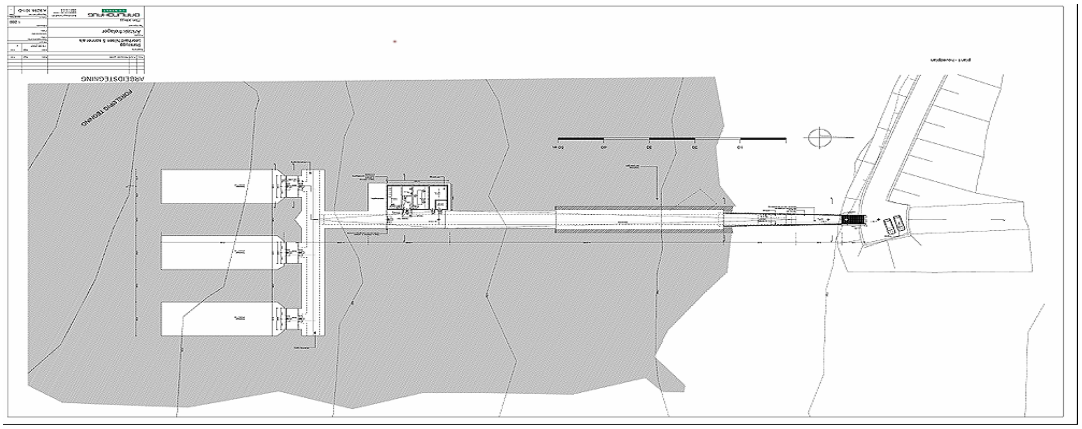

Fig. 2. The SGSV structure with the tunnel and three seed storage halls.

The organization

The organization of the SGSV reflects its international character and its long-term purpose for the whole world. Since Svalbard is Norwegian territory, the Norwegian government is the liable national authority. NordGen with its many years of experience with long-term storage and international work has the responsibility for the management and operation and sign the agreement with the depositors. The Global Crop Diversity Trust (GCDT) funds the operation and GCDT is also helping to secure operations by assisting

developing countries in the packing and dispatch of seed samples to Svalbard from eligible collections. Finally an International Advisory Council oversees the operation of the Vault, thereby ensuring that the SGSV is fulfilling its mandate and is meeting any unforeseen events according to the highest scientific expertise and in line with the international treaties.

How it all works – the terms of agreement

A number of terms apply for the seed-material placed in the SGSV and these are all specified in the depositor agreement signed by the depositors placing material in the SGSV. This agreement states, that:

- Storage in SGSV is free of charge for public and private holders of PGRFA;
- Shipment of seeds from developing countries will be supported by GCDT (while developed countries have to cover the shipment themselves);
- Material is stored in a Black box: meaning that it will never be opened and that the deposit of the seeds will not affect any property or other rights pertaining to the material;
- Viability testing, regeneration, and multiplication responsibility remains with the depositor;
- Information access is to be on public online data portal (SESTO);
- The depositor can on request at any time withdrawal the deposit; and
- The availability of the samples of accessions and non confidential information are regulated by Annex 1 of International Treaty (IT), Article 15.1(b) or Article 15.3 of IT or in case of none of these then terms and conditions that are substantially the same as Part IV of IT and applicable international agreements for material, which originated in the country of the depositor.

Status

The number of accessions stored in SGSV today (Oct. 2008) is 330,000 from more than 200 countries or regions. In particular, many large gene banks have deposited seeds in SGSV like CGIAR institutions (Fig. 3). Complements from local, national and regional gene banks are wanted and NordGen has send invitations for seeds depositing to all gene banks worldwide. The status with an overview of all deposited accessions in SGSV will continuously be up-dated on the website (*www.nordgen.org/sgsv/*).

Fig. 3. Preparation of the SGSV seed shipment

Conclusion

The experiences of the SGSV clearly show that to meet the challenges of securing the genetic resources of the world an active international collaboration and commitment is essential. The process can at times seem slow and painstaking, but the international collaboration and the framework for regulating this have progressed much during the last years. Also the political and financial will to provide the territorial location and the funding for the running costs and financial assistance to developing countries make a long-term storage project like the SGSV possible. The process has undoubtedly also been facilitated by the increasing public focus on the need to preserve the genetic resources of the world for the future. The media interest has been overwhelming. However, due to the vision of SGSV to be the most secure possible seed storage, the visiting policy has been very strict. In general, nobody except for the operators have entrance to Vault 2 where the seeds so far are stored. There is however, an informative model of SGSV with all relevant information in the Svalbard Museum open for everybody. The establishment of SGSV may be crucial in securing the plant genetic resources, but we have to remember that this is only one of the many steps needed to secure the future of mankind.

Standard Agreement between the Depositor and the Royal Norwegian Ministry of Agriculture and Food

Preamble

Whereas

1. The Government of the Kingdom of Norway has established the Svalbard Global Seed Vault to provide a safety net for the international conservation system of plant genetic resources, and to contribute to securing the maximum amount of plant genetic diversity of importance to humanity for long-term in accordance with the latest scientific knowledge and most appropriate techniques;

2. The Svalbard Global Seed Vault will be under the ownership of the Government of the Kingdom of Norway, and situated in Longyearbyen, Svalbard. The Royal Norwegian Ministry of Agriculture and Food is the national authority liable for the Svalbard Global Seed Vault;

3. The Royal Norwegian Ministry of Agriculture and Food, the Global Crop diversity Trust and the Nordic Gene Bank have entered into an agreement providing for the management, operation and long-term funding of the Svalbard Global Seed Vault. Under the agreement, the Nordic Gene Bank is required to liaise with depositors with respect to the material to be deposited and timetable and process for deposition, including guiding the depositors with regard to the packaging and labeling of the material to be deposited consistent with the guidelines and relevant national and international law, and is required, on behalf of the Royal Norwegian Ministry of Agriculture and Food, to enter into and sign the deposit Agreements with depositors on the basis of the Standard Deposit Agreement;

4. [**********] (hereinafter referred to as “the depositor”) holds a collection of seeds of distinct plant genetic resources of importance to humanity, and wishes to ensure the long-term safety of its collection by depositing samples of that collection in the Svalbard Global Seed Vault.

Now therefore, the Royal Norwegian Ministry of Agriculture and Food and the Depositor (hereinafter referred to collectively as “the Parties”) hereby agree as follows:

Article 1

Deposit of Plant Genetic Resources

1. The Depositor agrees to deposit in the Svalbard Seed Vault samples of plant genetic resources described generally in Annex 1 to this Agreement (hereinafter referred to as "the Deposited Materials"), and the Royal Norwegian Ministry of Agriculture and Food agrees to accept such deposit, in accordance with the terms and conditions set out in this Agreement.

2. The depositor recognizes the right of the Royal Norwegian Ministry of Agriculture and food to refuse to accept samples for deposit, or to terminate the deposit
   a. if the Depositor fails to comply fully with the terms and conditions set out in this Agreement; or
   b. for reasons of force majeure.

3. In particular and without prejudice to the generality of the above, the Depositor recognizes the right of the Royal Norwegian Ministry of Agriculture and Food to refuse to accept samples for deposit or to terminate the deposit of samples already deposited if the samples constitute duplicates of materials already held in deposit in the Svalbard Global Seed Vault.

Article 2

Effect of the Deposit on Property rights

1. The act of depositing the Deposited Materials in the Svalbard Global Seed Vault shall have no affect whatsoever on the nature and extent of any property rights pertaining to the Deposited Materials.

2. In particular and without prejudice to the generality of the above, the act of deposit shall not act in any way to convey any property rights over the Deposited Materials to the Nordic Gene Bank or the Royal Norwegian Ministry of Agriculture and Food.

Article 3

Obligations of the Depositor

1. Subject to paragraph 2 of this Article, the Depositor shall deposit only samples of plant genetic resources that
   a. are, to the best of the Depositor's knowledge,

i. of importance to food security and sustainable agriculture;

ii. the samples of plant genetic resources that have not yet been deposited in the Svalbard Global Seed Vault;

b. have been safety duplicated in a suitable genebank.

2. Any or all of the requirements set out in paragraph 1 of this Article may be waived by the Royal Norwegian Ministry of Agriculture and Food, or by the Nordic Gene Bank or other institution designated by the Royal Norwegian Ministry of Agriculture and Food to act on its behalf as manager of the Svalbard Global Seed Vault. Any waiver granted shall be in writing.

3. The Depositor shall provide an inventory of each shipment of Deposited Materials under this Agreement in accordance with the standards set out in Annex 2.

4. The Depositor shall ensure that Deposited Materials in each shipment:

a. conform fully to the general descriptions of the Deposited Materials in Annex 1 and to the specific descriptions in the inventory for that shipment;

b. are accompanied by any necessary certificates relating to the plant health of the samples as may be required by the laws of the country of export, the Government of the Kingdom of Norway, and any other country through whose territory the Deposited Materials are to transit, and that other procedures required by those laws in respect of that shipment have been complied with;

c. are deposited consistent with other relevant national and international law;

d. have been packed, sealed and labelled and are accompanied by appropriate documentation in conformity with the standards set out in Annex 2 to this Agreement, taking into account such guidelines as may be issued from time to time by the Royal Norwegian Ministry of Agriculture and Food; and

e. will be dispatched in accordance with the schedule set out in Annex 1 to this agreement.

Article 4

Conditions of Deposit

1. The material deposited will be maintained in permafrost conditions supplemented by refrigeration in accordance with internationally agreed standards for long-term seed storage.

2. All storage costs pertaining to the Deposited Materials shall, unless otherwise agreed between the Parties, be the responsibility of the Royal Norwegian Ministry of Agriculture and Food. Costs pertaining to the packaging and shipping of the Deposited Materials shall be borne by the Depositor.

3. The Deposited Materials will remain in sealed envelopes packed in sealed boxes, unless otherwise agreed with the Depositor. Where packages or boxes are damaged during transport or storage, or where packages or boxes have been opened for inspection by customs or other authorities, the Royal Norwegian Ministry of Agriculture and Food shall notify the Depositor. In the event that seeds have been spilled they will be destroyed. In the case of other damage the Royal Norwegian Ministry of Agriculture and Food will endeavour to repair the damage where possible, or provide for the repackaging or resealing of the Deposited Materials in consultation with, and with the agreement of, the Depositor.

4. The Royal Norwegian Ministry of Agriculture and Food will not accept responsibility for any germination testing of Deposited Materials, except as may be otherwise agreed in writing with the Depositor. The Royal Norwegian Ministry of Agriculture and Food will return testing samples of the Deposited Material for germination testing by the Depositor at the Depositor's request and expense, where such testing samples have been provided by the Depositor for that purpose in agreement with the Royal Norwegian Ministry of Agriculture and Food. Testing samples shall be packed in separate boxes.

5. The Royal Norwegian Ministry of Agriculture and Food shall inform the Depositor of the location of the Deposited Materials in the Svalbard Global Seed Vault.

Article 5

Withdrawal of Deposited Materials

1. The Depositor shall have the right to withdraw all or any of the Deposited Materials at any time on the giving of written notice.

2. Any written notice given under this Article shall identify the individual boxes of Deposited Materials that are to be withdrawn. No Deposited Materials will be returned where this requires the opening of a box or boxes in which the Deposited Materials are packed.

3. The Royal Norwegian Ministry of Agriculture and Food undertakes to return the Deposited Materials within a period of one year from the date of receipt of such written notice.

4. The costs of packaging and shipping in respect of the return of Deposited Materials shall, unless otherwise agreed between the Parties, be borne by the Depositor.

5. The Depositor shall be responsible for complying with all export clearance procedures required by the Government of the Kingdom of Norway of the Deposited Materials and for all import or transit procedures required by the country of import or transit. The Royal Norwegian Ministry of Agriculture and Food shall use its best efforts to provide such documentation regarding the Deposited Materials and the conditions under which the Deposited Materials were deposited as may be necessary to facilitate such procedures.

6. The Depositor shall notify the Royal Norwegian Ministry of Agriculture and Food in writing if it wishes the Deposited Materials to be no longer retained in the Svalbard Global Seed Vault but does not wish the Deposited Materials to be returned to it; in such case, the Deposited Materials will be disposed of by the Royal Norwegian Ministry of Agriculture and Food in accordance with its operating rules and procedures applicable to the Svalbard Global Seed Vault.

Article 6

Right of the Royal Norwegian Ministry of Agriculture and Food to Terminate the Deposit

1. The Royal Norwegian Ministry of Agriculture and Food shall have the right to terminate the deposit, or part thereof, on the giving of one year's written notice, where such termination is required as the result of any change in the policy of the Svalbard Global Seed Vault or the Government of the Kingdom of Norway with respect to the Svalbard Global Seed Vault.

2. Where Deposited Materials are returned as a result of the exercise by the Royal Norwegian Ministry of Agriculture and Food of its right of termination under this Article, the costs of packaging and shipping in respect of the return of Deposited Materials shall be borne by the Royal Norwegian Ministry of Agriculture and Food.

Article 7

Availability of Plant Genetic Resources

1. In consideration for the right to deposit samples of plant genetic resources in the Svalbard Global Seed Vault, the Depositor agrees to make available from their own stocks samples of accessions of the deposited plant genetic resources and associated available non-confidential information to other natural or legal persons in accordance with the following terms and conditions:

   a. Where the plant genetic resources are plant genetic resources for food and agriculture of crops listed in Annex 1 of *the International Treaty on Plant Genetic Resources for Food and Agriculture* [hereinafter referred to as "the Treaty"], in accordance with the terms and conditions set out in Part IV of the Treaty; or

   b. Where the plant genetic resources are plant genetic resources for food and agriculture covered by Article 15.l.(b) or Article 15.3 of the Treaty, in accordance with the terms and conditions provided for in Article 15.l(b) or Article 15.3 of the Treaty, as the case may be; or

   c. Where the plant genetic resources for food and agriculture are not of crops listed in Annex 1 of the Treaty or covered by Article 15.l (b) or Article 15.3 of the Treaty, either:

      i. In accordance with terms and conditions that are substantially the same as the terms and conditions set out in Part IV of the Treaty; or
      ii. Where the plant genetic resources for food and agriculture originated in the country of the Depositor, and are not available for facilitated access under the terms of the Treaty, in accordance with the provisions of applicable international agreements.

   d. Where the plant genetic resources are not plant genetic resources for food and agriculture, in accordance with the terms and conditions set out in paragraph c. above as appropriate.

2. The Royal Norwegian Ministry of Agriculture and Food reserves the right to give the highest priority to the safety storage of plant genetic resources for food and agriculture that are available in accordance with the terms and conditions set out in Part IV or Article 15 of the Treaty or terms and conditions that are substantially the same as those terms and conditions.

Article 8

Liability

1. The Royal Norwegian Ministry of Agriculture and Food shall not be liable for any damage caused to the Deposited Materials by any reason whatsoever, unless such damage has been caused as a result of any act of malfeasance or negligence on the part of the Royal Norwegian Ministry of Agriculture and Food or any employee or agent of the Royal Norwegian Ministry of Agriculture and Food.
2. In the event of any damage caused by malfeasance or negligence on the part of the Royal Norwegian Ministry of Agriculture and Food or any employee or agent of the Royal Norwegian Ministry of Agriculture and Food, the liability of the Royal Norwegian Ministry of Agriculture and Food shall be limited to the costs of packaging and shipping of new samples, and shall not include costs of regeneration of the plant genetic resources, or similar costs.

Article 9

Amendment

1. This Agreement, including the annexes to this Agreement, may be amended by mutual written agreement of the Parties.
2. Any amendment shall enter into force on the date provided for in the amending agreement.

Article 10

Entry into Force

This Agreement shall come into force on its signature by the authorized representatives of both the Depositor and the Royal Norwegian Ministry of Agriculture and Food.

Article 11

Duration of the Agreement

1. This Agreement shall remain in force for a period of ten (10) years and shall be renewed automatically for further periods of ten (10) years unless either Party gives notice in writing to the other Party at least six months prior to the expiry of any ten (10)

years period that it does not wish this Agreement to be renewed.

2. This Agreement may be terminated by mutual agreement between the Parties to this Agreement.

Article 12

Settlement of disputes

1. Any dispute that cannot be settled by negotiations between the Parties to this Agreement, or through such other procedure as may be agreed between the Parties, shall be finally settled by arbitration in accordance with the Rules or Arbitration of the International Chamber of Commerce by one or more arbitrators appointed in accordance with the said Rules.
2. This Agreement shall be governed by the laws of the Kingdom of Norway.

Article 13

Signature

This Agreement will be signed in three copies.

Signed on behalf of the Depositor:	**Signed on behalf of the Royal Norwegian Ministry of Agriculture and Food:**
_____	_____
Signature	**Signature**
_____	_____
Name	**Name**
_____	_____
Title	**Title**
_____	_____
Date	**Date**

Annex 1

General Description of the Deposited Materials

Depositors are required to provide the following information describing their planned deposit of materials under the Agreement.

Provide a listing of the genera/species and crop to be deposited

- Provide the approximate total number of samples and the approximate number by crop
- Provide a provisional schedule for the deposit shipments, giving the approximate month and year of each shipment and the approximate number of samples per shipment

The information should be provided in the following tabular format:

Crop/Species	**Month/2008**	**Month/Year**	**Month/Year**	**Month/Year**	**etc.**	**Total**
Wheat	10,000*	5,000	etc.			
Rice						
etc.						
Total						100,000

* Number of samples

- Provide any additional information that the Royal Norwegian Ministry of Agriculture and Food may request in order to be able to arrange the deposits.

Annex 2

Requirements for the Quality, Quantity, Packing, Inventory, and Shipment of Deposit Materials

2. The samples of plant genetic resources for food and agriculture (PGRFA) must be of seed of high viability, free from diseases and pests as far as possible, and able to maintain adequate levels of germination for at least 10 years.

3. Each sample should contain sufficient seeds to maintain the genetic integrity of the accession of PGRFA through at least two independent regenerations. In general, this may require a sample size in the order of 500 seeds; however actual sample size shall be at the discretion of the Depositor in accordance with latest scientific best practice.

4. The seed samples must be packed and sealed in laminated aluminum foil packets. The foil packets must be durable and impervious to moisture, and generally conform to standards recommended for low temperature seed storage. Where packets contain sharp seeds, appropriate linings must be used to minimize the risk of puncturing the packets.

5. Each seed packet must be labelled with the Depositor's accession identifier/number for the PGRFA in question. Labels must be durable under the conditions of long-term low temperature storage.

6. The seed packets must be packed and sealed in deposit boxes. The boxes must be durable, constructed of a material that is strong enough to support the weight of the seed packets they contain, withstand handling during shipping and remain rigid during cold storage, and generally conform to standards recommended for low temperature storage.

7. A deposit box should be filled with samples that are expected to have the same life span (ie. are of the same species and regeneration cycle), thus in general needing replacement at the same time.

8. Each deposit box must be labelled with the Depositor’s name and box identification number. Labels must be durable under the conditions of long-term low temperature storage, and must be placed on the top and four sides of the box.

9. The deposit boxes must have an external dimension no greater than 60cm long by 40cm wide by 28cm high and no less than 55cm long by 35cm wide by 25cm high. Where deposit boxes of a smaller dimension are necessary (see point 6) then two but no more than three deposit boxes may be placed in a storage box that conforms with required maximum and minimum dimensions. In these cases the outside box munt also be labeled with the Depositor's name and the identification numbers for the deposit boxes inside.

10. Any boxes of testing samples for germination checking (as may have been agreed with the Nordic Gene Bank) must be clearly marked accordingly.

11. All deposit boxes must include a list of their contents within the sealed box. The list must provide at the minimum the following information for each seed sample in the box:
    – the Depositor’s accession number/identifier;
    – the crop and full scientific name;
    – the country of collection or source;
    – the number of seeds in the sample; and
    – the month and years of regeneration.

12. For each planned shipment of Deposit Materials to the Svalbard Global Seed Vault (as described in Annex 1):

- Notice of the deposit must be confirmed to the Nordic Gene Bank at least six weeks in advance of the planned date of shipping. This notice must include an electronic inventory of the contents of all the deposit boxes in the planned shipment. The inventory should include the Depositor’s name, the deposit box numbers and for each deposit box the data required on the contents as listed under paragraph 10. In general, the electronic inventory should conform to data standards widely used for inventorying PGRFA collections and to the data template provided by the Nordic Gene Bank.
- Following receipt of confirmation from the Nordic Gene Bank that the deposit can proceed and the import document for Svalbard, the shipment should be made by air courier to Longyearbyen, Svalbard following the fastest and most direct routing, where possible avoiding transit through airports where temperatures are high.
- All shipments must conform to the requirements set out in this Annex and any additional guidelines provided by the Nordic Gene Bank, and include all necessary export, phytosanitary and import documentation.

- The shipment must be addressed to:
  The Svalbard Global Seed Vault
  The Governor of Svalbard
  PO Box 633
  9171 Longyearbyen
  Svalbard
  Norway

- Further information can be sought from:
  The Coordinator for the management of the Svalbard Global Seed Vault,
  The Nordic Gene Bank
  PO Box 4 1
  Smedjevägen 3, Alnarp
  S-23053 Alnarp
  Sweden
  Tel: +46 4053 6640
  Fax: +46 4053 6650
  www.nordgen.org/ngb

Data Submission Template for the
Svalbard Global Seed Vault (SGSV)

The spreadsheets below are the data submission template for the Svalbard Global Seed Vault (SGSV). You will find here two template sheets for data entry: Accessions and Institutions. The template sheet for reporting data about the accessions is mandatory. The template sheet for reporting additional information about institutes is optional.

You may want to report the inventory of the seeds in your shipment in another data format. Currently supported data formats include tab-separated text (txt), comma separated values (CSV) and XML data. Please contact the staff at SGSV if you have other favorite data formats you wish to use when reporting your inventory of seeds.

A data portal for the Svalbard Global Seed Vault (SGSV) is now available online from the link below. From the SGSV data portal you will find a tool to submit this template spreadsheet online. For access and permissions to this online tool to upload your template you will be provided with a personal password. You may also send your completed data submission template by email addressed to the staff at the SGSV (sgsv@nordgen.org).
http://www.nordgen.org/sgsv/

Depositor (contact data for the seed shipment)

The contact data for all seed depositors will be registered at the data portal site. The registered seed depositors will be able to update their own contact data at the portal web site, authenticated by a personal password. Please include at least one contact person and email address to be used by the SGSV to make contact about the seed shipment or for later correspondence about the deposited box.

Accessions (list of seeds in the shipment)

Please use the format of the SGSV data submission template to report your inventory of seed accessions you want to send to the Svalbard Global Seed Vault. Please note that the descriptors for Institute code, Collection name, Accession number, Full scientific name, Country of collection or source, and Regeneration month and year are mandatory.

Accessions: Descriptors

Institute code	WIEWS Institute Code (INSTCODE) for the institute holding the genebank accession. (You may access the WIEWS institute database at *http://apps3.fao.org/wiews/*)
Deposit box number	Give each box in your shipment a unique number, and record here those numbers.
Collection name	If your genebank uses parallel numbering systems for different collections, give here the name of the collection, e.g. Bean Collection.
Accession number	Please make sure that the combination of Institute Code, Collection name and Accession number is globally unique.
Full scientific name	*Genus species subspecies,* including authority and year of description if available.
Country of collection or source	Where the accession is originally from. Please use ISO-3166-1 (alpha 3) country codes if possible.
Number of seeds	This number can be based on a full count or on an estimate from the weight of the sample.
Regeneration month and year	The harvest year is mandatory to be able to identify the regeneration cycle of the seed sample. (Examples: 2005, 2005-10-08)
Other accession designations	You may report other accession designations here (L.e. accession number for the same accession in another genebank). A semi-colon should separate each designation.

Institutions (if needed, additional information about referred institutes)

You may report additional data on institutions using the template sheet labeled "Institutions". Please note that a valid WIEWS Institute Code (FAO's World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture) is required for the holding genebank institute. This sheet for the Institute data is voluntarily, if all the institutes you refer to are described by the WIEWS Institute Code (INSTCODE) the data you report here need not be used.

APEC-ATCWG Workshop (2008)
Capacity Building for Risk Management Systems on Genetic Resources
21~34

Preserving the Future of Vegetable Improvement

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Abstract

Diverse and readily accessible genetic resources are vital for any crop improvement program oriented toward high and stable yields and specific consumer preferences to finally contribute to food security and a diverse diet for the ever increasing global population. Molecular tools to identify and use genes responsible for specific traits in gene bank accessions of wild and cultivated species have great potential to enhance germplasm utilization and to shorten breeding cycles. Complementary approaches of *in situ* and *ex situ* conservation are used to preserve germplasm for improvement programs. AVRDC – The World Vegetable Center conserves approximately 56,000 accessions and is therefore the world's most important gene bank for vegetable crops. More than 35,000 samples of regular and improved vegetable germplasm have been distributed over the last 10 years to a range of users in the public and private sectors. Another 10,000 samples have been used by the Center's scientists for their research. After extensive screening and breeding efforts, five anthracnose-resistant pepper lines have been released by the Center. Similarly, *Solanum pimpinellifolium*, a wild tomato species is being used to develop resistant varieties against bacterial wilt. Resistance against the damage from aphids was detected in *Capsicum annuum* accessions from Costa Rica. Moderate to highly resistant lines to bruchid, a destructive storage insect pest of mungbean resulted from extensive screening trials at the Asian Regional Center. The AVRDC Vegetable Genetic Resources Information System (AVGRIS) provides direct access to information pertaining to the accessions in the gene bank to all potential users through the internet. To secure the future of variety improvement programs of staple crops including fruits and vegetables, gene bank capacities for medium to long-term

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conservation, germplasm characterization and evaluation, and information exchange need to be given priority attention.

Introduction

The foundation of the current world food supply is based on thousands of years of crop selection and improvement carried out on traits of wild species (McCouch, 2004). The present-day cultivated breeds are descendants of wild species which had low yields and poor eating quality, but nevertheless provided the modern varieties with genes that can enhance crop performance. Over 60 years ago, Vavilov drew attention to the potential of crop relatives as a source of genes for improving crop performance (Vavilov, 1940, as cited by Tanksley & McCouch, 1997). This possibility motivated the setting up of gene banks which initially were focused on species that are closely related to 'exotic' crops. However, the future productivity of all agricultural crops – both exotic and local – can only be ensured if collection and preservation of genetic variation in genebanks is tied in with active utilization of the materials in the collection (Tanksley & McCouch, 1997).

There is no a single country that is self-sufficient in genetic resources for food and agriculture. All countries greatly depend on plant genetic resources for food and agriculture from other parts of the world for their food production and sustainable agricultural development. Concern over the dramatic loss of agrobiodiversity in farmers' fields and in nature has led to efforts to conserve plant germplasm in several *ex situ* collections maintained by national and international research centers throughout the world. According to FAO, approximately 6.1 million accessions of plant genetic resources for food and agriculture are currently stored in over 1400 recorded genebanks around the world (Hodgkin and Anishetty, 1998).

Genetic resources are vital for the world's future. All living things exist in a range of forms and types and this diversity must be preserved. Collecting and conserving this diversity in a form that will serve for current and future use for food and other purposes is essential for the survival of mankind. In terms of botanical diversity, there are around 400,000 known species of plants (*www.bgci.org/conservation*) and many are yet awaiting to be described. However, of this tremendous biological diversity, only a small number of species is currently preserved in *ex situ* or *in situ* collections of plant genetic resources. The Kew's Millennium Seed Bank worldwide collaboration, for example, only aims to safeguard approximately 24,000 plant species (Kew's MSB, 2004).

Issues on germplasm conservation, sharing and use

Plant genetic resources have been collected for different reasons over the last centuries. Often collections are held for specific commercial uses, for example, the collection of cocoa genetic materials maintained by the Malaysian Cocoa Board (Carrizosa, 2004) is meant to support commercial cocoa production at a national level. Other collections have been initiated for more academic or philosophical reasons such as the collections made by Linnaeus stored in London by the Linnean Society and by Darwin, housed at the Natural History Museum, London.

In more recent times there has been increasing concern over the status of the world's plant genetic resources in relation to humanitarian, commercial, intellectual property and environmental issues. Humanitarian concerns are particularly linked to possible losses of genetic materials resulting from civil unrest (for example the civil war in Cambodia, the military conflict in Darfur, Sudan, or the religious conflict in the Mollucan islands, Indonesia). Varieties or specific, locally adapted types may be lost forever in the wake of civil unrest. In some cases it has been possible to repatriate genetic materials to their countries of origin through the use of genetic resources collections, enabling those countries to restore the natural crops and cropping patterns of the area. Some examples of these efforts are: the reintroduction of various rice varieties in Cambodia by the International Rice Research Institute (Pearce, 1998), and the repatriation of indigenous crop varieties to Afghanistan by the Future Harvest Consortium led by the International Center for Agricultural Research in the Dry Areas (*www.icarda.org*). The largest effort to repatriate local seed to date is probably the "Seeds of Hope" project, an international joint venture launched to restore agricultural biodiversity in war-torn Rwanda (CGIAR, 1996).

Commercial interests are very broad and often historically linked to patterns of human movement and needs for food, or medicinal or industrial purposes. Genetic resources have been vital in developing new and improved lines of crops and also for ensuring diversity in the human diet. High lycopene and beta carotene tomatoes, for example, provide more antioxidants and vitamin A than the regular varieties. Many of the world's medicines are derived from plants. It is reported that approximately 25% of all the world's medicines are derived from 10,000-20,000 plant species (Duke, 1993).

Ownership of traditional plant genetic resources, equitable sharing of benefits arising from their use, and emerging national plant variety protection laws are intellectual property

issues affecting the way those resources are currently collected, exchanged and utilized. The United Nations' Convention on Biological Diversity and the International Treaty on Plant Genetic Resources for Food and Agriculture (FAO, 2001) are international agreements with the aim to ensure that plant genetic resources are conserved and remain available to mankind while recognizing sovereign rights of the countries from which the plants originated.

Environmental issues are also becoming increasingly important, as issues of climate change are discussed internationally. The impacts of climate change on natural environments could result in the loss of genetic diversity from areas which experience major environmental or climatic disturbances. Changes in seasonal variability, ambient carbon dioxide concentration, rainfall amount and distribution and air temperature will have a major impact globally. In addition, the effects of natural disasters such as the Indian Ocean's 2004 Tsunami; the 2008 earthquake in Sichuan, China, hurricane "Nargis" in Myanmar, and the monsoon flood in Bihar, India, for example, on the loss of local plant species cannot be underestimated.

Value of genetic resources in crop improvement

Genetic improvement is vital for ensuring food security in an ever increasing global population. Traditional varieties or land races originated as low yielding, relatively weedy species that had undergone natural selection and farmers' selection processes for thousands of years. New varieties have been developed through conscious efforts of plant breeders who are targeting not only yield and stabilizers of yield performance (resistance to abiotic and biotic stresses) over time but also consumer preferences, whether in terms of taste, color, storability, postharvest processing attributes or nutritional values.

To a large extent, the success of any crop improvement work depends on the genetic diversity available to the breeders. The more diverse and readily available the genetic resources are, the better the chances that the genetic improvement efforts will provide the desired plant characteristics. All genetic improvement requires an existing base of genetic material which is modified using conventional plant breeding and/or molecular genetic techniques. The latter could involve application of molecular marker aided selection and/or insertion of a specific gene to produce a genetically modified variety. Examples of the genetically-modified crop include rice with high beta-carotene content and herbicide-resistant soybeans.

The application of molecular tools to identify genes controlling specific traits in accessions of cultivated species and their wild relatives constitutes an important new role of gene banks to enhance germplasm utilization. The introgression of identified genes into genotypes with a more desirable genetic background using marker-assisted selection (MAS) has been a component of this approach (Tanksley and Nelson, 1996; Xiao *et al*., 1996; Ortiz and Engels, 2004). As an example, the MAS scheme discussed by Causse *et al*. (2001) for the transfer of the five most important QTLs involved in the organoleptic fruit quality of tomato can be mentioned.

The analysis of genetic variation in germplasm collections and the proper documentation of the number and types of useful polymorphisms provide opportunity to estimate the value of the conserved accessions and enable the gene bank to offer specific accessions with desired characteristics to plant breeders and users in general. They can then make informed choices and select only those genotypes which best fit their objectives (Ortiz and Engels, 2004).

The rate of discovery of nucleotide variation at QTLs contributing to phenotypic variation of complex traits is expected to increase with the adoption of linkage disequilibrium and candidate gene strategies for QTLs fine mapping and cloning (Rafalski, 2002; Morgante and Salamini, 2003). This approach would eliminate the requirement for structured segregating populations and genetic studies could be directly performed on the accessions deposited in the genebank (Graner *et al*., 2004). The feasibility of association mapping between DNA markers and agronomic traits has been successfully demonstrated in a genebank collection of 600 potato varieties. Highly significant association with QTLs for resistance to late blight and plant maturity was detected with PCR markers, specific to a major gene for resistance to late blight (Gebhardt *et al*., 2004).

Developing these ideas further, DNA banks may evolve as a strategic component of modern gene banks providing the basis for improved gene bank management and facilitating high throughput germplasm characterization, association genetics and marker-assisted selection. DNA samples can be exchanged much easier and at lower costs than living plant materials, without the inherent risk of spreading diseases and pests (Ebert *et al*., 2006). In addition, DNA banks may serve as reference basis for evolutionary and comparative genomic studies and may offer a complementary conservation strategy for species under threat of extinction. They can also serve as safety duplicate for the physical seed, field or in vitro collections, although it is not yet possible to regenerate plants from stored DNA.

In situ and *ex situ* conservation of genetic resources

Genetic resources include wild and domesticated species, landraces, advanced breeding lines and improved varieties. Collecting expeditions, sharing of genetic resources between gene banks, and the assembly of advanced breeding lines and improved materials are important pillars of crop germplasm collections held in gene banks.

Conservation of genetic resources can be *in situ*, at the plant's natural habitat (e.g. Yayu-Harumu region in Ethiopia to conserve diversity of Arabica coffee, *Coffea arabica* [Abebaw and Virchow, 2003]) or *ex situ*, outside their natural habitat, such as in gene banks or botanical gardens. *Ex situ* conservation consists of a number of different methods, including seed storage, *in vitro* and cryopreservation, the maintenance of living plants in field gene banks and pollen storage. *Ex situ* seed collections are usually stored at +5 ^{o}C or less than 0^{o}C for short to medium-term storage (active collections) and at approximately –18 ^{o}C or less for long-term storage (base collections). The aim of *ex situ* collections is often long term storage including safety back-up of valuable accessions at other gene banks to reduce risks of genetic erosion or complete loss due to biotic or abiotic effects or natural disasters. All forms of *ex situ* conservation offer the possibility of reintroduction of the plants into their natural habitat.

Both types of conservation have different roles. *In situ* collections are generally used to conserve species diversity within natural habitats and ecosystems where populations of plants naturally exist, while *ex situ* conservation provides opportunities for characterization, evaluation, documentation, and supply of germplasm to users and other gene banks.

There are many other criteria which must be observed to ensure longevity of the seed collections, including appropriate physiological maturity of the seeds, absence of mechanical damage, adequate seed processing and drying, good health status and purity of the seeds, low seed water content, packaging in impermeable containers or bags, low storage temperatures, periodic viability controls and rejuvenation of seed lots when viability has declined.

Genetic resources at AVRDC – The World Vegetable Center

Vegetable genetic resources are a very important global asset, given that micronutrients and bioactive compounds which are important in human diet are found in

vegetables. This increasing recognition of the important role of fruits and vegetables in nutrition and health has increased interest in the preservation of genetic resources to support vegetable improvement. It is particularly important to locate and conserve underutilized species and types, often known as indigenous vegetables. Indigenous vegetables include species that are native to a particular region or introduced historically to a region from other areas, such as nightshade, tropical violet and amaranth. Other vegetables such as carrot, onion or tomato, which have been grown and enjoyed in almost all regions in the world, are generally considered exotic vegetables.

Vegetable genetic resources are assembled by both the private and the public sectors. The private sector collections include collections of brassicas (China Long, Taiwan), tomatoes (Tomato Fest Organic Heirloom, USA), and various other vegetables (Sakata, Japan) whereas the public sector collections include among other vegetables, *Brassica* (2262 accessions) and tomato (approximately 5000 accessions) collections held by the US Department of Agriculture, the C.M. Rick Tomato Genetics Resource Center located at the University of California in Davis with approximate 3000 accessions, most of which are genetic mutants or wild genotypes (Mueller, 2007). The Tropical Agricultural Research and Higher Education Center (CATIE) at Turrialba, Costa Rica conserves a total of 4753 accessions of vegetable crops with cucurbits, chili pepper and tomatoes constituting the major crops. AVRDC – The World Vegetable Center conserves a total of 56,000 accessions and is therefore the world's most important gene bank for vegetable crops.

Vegetables are generally stored as true seed (e.g. eggplant, cabbage, cucumber, tomato, cucurbits, chili pepper), however some species must be maintained as vegetative propagules (such as onion, garlic and shallot).

Vegetable germplasm collecting

Germplasm conserved in the Center's genebank are collected through many ways. Most of the collection came from national partners and other institutes' voluntary and requested contributions. Many friends of the Center staff became donors of traditional cultivars. While conducting research activities, scientists are not only utilizing the existing genetic resources collection, but also add to the collection from the germplasm they acquire through research projects and from results of their breeding activities. These processes of germplasm collections are invaluable, but the exact cost is difficult to estimate. In addition, there are efforts or expeditions designed specifically toward germplasm collection. An

example of such is the Center's ADB-funded project in Asia which successfully collected 4326 accessions of indigenous vegetable germplasm, most of them are generously contributed by farmers from various locations in eight participating countries. Germplasm collecting activities of the Center follow international agreements and national laws.

Vegetable germplasm preservation

AVRDC – The World Vegetable Center holds the world's largest non-private sector collection of vegetable genetic resources. Genetic resources from around the world are conserved at its Genetic Resources and Seed Unit (GRSU) in Shanhua, Taiwan. In addition, the Center also has a working collection and short-term storage facilities at its Regional Center for Africa in Arusha, Tanzania.

The facilities at GRSU are suitable for short- (15 ^{o}C, 40%~45% RH), medium- (0~5 ^{o}C, 40%~45% RH) and long-term (–16 to –20 ^{o}C) storage and in-vitro conservation. In addition to seed processing facilities such as cleaning, drying and packing, the genebank also maintains regeneration and experimental facilities. The gene bank conserves 394 different species from 150 countries, making it one of the largest collections of vegetable germplasm held by a single institution. The storage facilities in Arusha, Tanzania comprise mainly +5 ^{o}C refrigerators for short-term storage of accessions and working collections. The Arusha collection comprises of 304 accessions of vegetable germplasm, most of which are species indigenous to Africa.

AVRDC – The World Vegetable Center also stores for safekeeping duplicate samples of vegetable germplasm collections of individual countries. In addition, the Center collections are partly safety duplicated at the Taiwan's National Plant Genetic Resources Center, the gene bank of the Ministry of Agriculture of Japan, the Philippine National Plant Genetic Resources Laboratory, the UK's vegetable gene bank in Wellesbourne, the US National Germplasm Resources Laboratory in Beltsville, and Norway's Svalbard Global Seed Vault, the last one being a black-box storage.

Vegetable germplasm sharing.

The processes of collecting, characterization and storage of the collections of vegetable germplasm held at AVRDC – The World Vegetable Center are a continuing activity. The Center's gene bank concentrates on the conservation of globally important vegetables,

and those that are important in South Asia, Southeast Asia, and Africa. Its activities are conducted using standard protocols following the internationally recognized best practices. Although the Center's gene bank's main aim is conservation, it is also utilization-oriented: its base collection is complemented with a well utilized active collection. The Center strongly believes that while the material is stored to ensure its availability in the future, it is very important that the material is used. To enhance utilization of germplasm, the Center's gene bank regularly distributes both improved and unimproved vegetable germplasm to both public and private sectors. More than 35,000 samples have been distributed over the last 10 years to government- and non-governmental organizations, public and private seed companies, and private individuals. Another 10,000 samples have been used by the Center's scientists for their research. In 2007 alone, more than 4000 samples or 25% of the 16,279 total samples of various crops distributed by the Center worldwide were accessions from this genebank. Of this number, 29% or 1298 samples went to the regional centers and the various units at Headquarters. The rest were distributed to government and nongovernmental organizations, universities, seed companies, and private individuals in over 60 countries.

Vegetable germplasm utilization

Genetic diversity is the foundation of any varietal improvement program, with international crop centers serving as the modern centers of genetic diversity. Many wild relatives of cultivated plants possess better traits to withstand biotic and abiotic stresses than its cultivated counterpart. These wild species, however, lack the characteristics that are sought for human needs and use, such as fruit size, organoleptic traits, or shelf-life. Screening of diverse germplasm from international centers for desirable agricultural attributes is a valuable breeding endeavor. Selected materials can be used directly as varieties or parents in breeding programs.

At the Center's headquarters, resistance to Anthracnose (*Colletotrichum* spp.) in pepper (*Capsicum* spp.) was sought in an extensive survey of the Center's *Capsicum* germplasm collection, and a small number of promising accessions in *Capsicum chinense* (e.g. PBC932) and *Capsicum baccatum* (PBC80 and PBC81) were identified. The resistance was transferred into *Capsicum annuum* via interspecific hybridization and several backcrosses, utilizing a micro-injection screening protocol also developed by the Center. The gene controlling this resistance has been tagged using AFLP methods, and improved SCAR markers are currently being developed. Beginning in 2003, at least five resistant lines

incorporating this resistance factor have been bred by the Center, and made available to interested researchers.

The wild tomato species *Solanum pimpinellifolium* is highly resistant against bacterial wilt caused by *Ralstonia solanacearum*, but its fruit size is very small and it has poor horticultural traits. The resistance genes from *S. pimpinellifolium* were incorporated into a cultivated recipient parent and a highly resistant commercial tomato variety, Hawaii 7997 was produced (Hanson *et al*., 1998). *S. pimpinellifolium* is one of many wild species being used at the Center for breeding activities, aimed to produce varieties with better characteristics.

The Center recently screened over 100 lines of *Capsicum annuum* originating from Costa Rica and maintained in the GRSU collection, for resistance to damage from aphid (*Myzus* spp.). Six lines were identified that display damage levels of less than 10% the trial average. At the Center's Asian Regional Center, 611 mungbean accessions have been screened for resistance to bruchid (*Callosobruchus chinensis*), a destructive storage insect pest that bores inside and feeds on bean pods. Seven accessions with moderate to highly resistant reaction to bruchid have been identified. All these accessions can be requested from the Center by vegetable breeders.

As part of the Center's okra breeding activity in West Africa, 68 lines of okra (*Abelmochus esculentus*) from the Center's genebank together with 76 accessions introduced from the National Plant Germplasm System, Griffin, Georgia, and USA were characterized; seeds were increased and evaluated for general adaptation in Niger during the rainy season of 2008. Promising lines will be selected and crossed with small-fruited *A. manihot*.

Some other genes which have been mined and incorporated into the Center's vegetable lines include heat tolerant genes in Chinese cabbage and yellow leaf curl virus resistance genes in tomato. There are also advanced breeding lines of major vegetable crops that are tolerant to flooding and drought and are efficient in nitrogen-use.

Documentation and information sharing

AVRDC Vegetable Genetic Resources Information System (AVGRIS) is the computer-based information system developed and maintained by AVRDC's genebank staff to facilitate the daily maintenance and use activities. It links all gene bank operations associated with germplasm conservation and management. The information system is used

in the recording, storing and maintenance of germplasm data, such as passport, characterization and seed inventory data. More importantly, it provides direct access to information pertaining to the accessions in the gene bank through the internet.

Information of the Center's genetic resources on AVGRIS is available through the internet (*www.avrdc.org*). These genetic resources maintained by AVRDC in-trust are considered as international public goods and are provided on agreement with the terms of the Center's Material Transfer Agreement.

Meeting the needs of the future

The availability of genetic materials in the gene bank provides a wealth of opportunities for the Center to be well positioned in tackling problems of pests and diseases as well as issues of climate change and extreme weather events in vegetable production. It underlines the importance of maintaining the Center's Genetic Resources and Seed Unit for the preservation of vegetable genetic resources diversity and to enhance its utilization for food and nutritional security.

The Center's Genetic Resources and Seed Unit is funded through contributions to the Center as an international research and development center. Funding is both from the unrestricted core funds and from designated donor-funded projects. An annual budget of approximately US$ 450,000 is needed to run and maintain the Genetic Resources and Seed Unit at the Center's Headquarters in Taiwan. The Genebank Manager supervises nine regular staff and 5~10 field laborers to manage the day to day operation of the gene bank. The storage facility in Tanzania is managed by three staff and five laborers with an annual budget of approximately US$ 150,000. The personnel cost comprises of more than 80% of the annual budget. Greenhouse and laboratory operations for regeneration, characterization, seed multiplication, etc., take up about 7%~8% of the annual cost. The infrastructure, operation cost for electricity, water, and its maintenance come next, followed by cost of packing and shipping for distribution and to backup the collection. Data base maintenance and its accessibility are another very important part of the gene bank operation involving two technical staff to keep the information up-to-date.

The establishment of international agricultural research centers dealing with important crops (AVRDC – The World Vegetable Center, International Rice Research Institute, Centro Internacional de Mejoramiento de Maiz y Trigo, International Crops Research Institute for the

Semi-arid Tropics, and Centro International de Agricultura Tropical, to mention a few) has led to worldwide efforts on genetic resources conservation, sharing and utilization for center-mandated crops. Today, the gene banks of these international centers are the primary sources of crop germplasm for valuable traits for adaptation, stability and human health. To secure the future of variety improvement programs for food and agriculture of all nations, like vegetable variety improvement, there is a need to sustain and expand the gains in crop genetic resources conservation programs of international centers that hold these resources in-trust for the world community. Germplasm collecting in less accessible areas should be done to avoid genetic erosion due to rapid urbanization, civil unrests and/or drastic global climate change. International gene bank capacities for medium to long-term conservation, germplasm characterization and evaluation, and information exchange should be given priority attention.

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Management of Germplasm Collections and Enhancing Their Use by Mini Core and Molecular Approaches

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Abstract

Genetic resources provide basic material for selection and improvement through breeding to ensure food security needs of the world's rapidly raising population. Conservation and utilization of plant genetic resources are important components of *ex situ* collections. The establishment of large, germplasm collections at ICRISAT genebank, Patancheru, India, was based on donations from existing collections. This was augmented by targeted germplasm collection missions. Majority of them are orthodox seed producing accessions. The conserved germplasm accessions have been characterized for important morpho-agronomic characters and germplasm seed samples are distributed to bonafide researchers for utilization in crop improvement programs all over the world. Exiguous use of germplasm has been observed in breeding programs, mainly due to lack of information on economic traits. Core collections and mini core collections have been developed to enhance use of germplasm in breeding programs globally. The core and mini core collections were evaluated to identify genetically diverse trait specific germplasm for resistance to abiotic and biotic stresses and for agronomic traits for use in breeding programs to develop broad based cultivars. Molecular characterization of composite sets of germplasm, that include core or mini core collections, have helped in understanding genetic diversity and population structures in each species. Genotype based reference sets of genetically diverse 300 accessions have been established. Seeds of mini core collection and reference sets are available for use by the global research community.

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Introduction

Domestication of plants began long ago when the nomadic human beings turned from gatherers to growers and started cultivating plants of their choice for food and other needs. Crop diversity is part of the biological diversity and includes the resources that contribute to people's livelihoods by providing food, feed, medicine, fiber, clothing, shelter and energy. Hence, it contributes towards achieving the global objectives of food security, poverty alleviation, environment protection, and sustainable development. Crop diversity is a major component of crop improvement and is required for both short-term and long-term food security and to increase productivity and reduce malnutrition.

Over the years, genebanks have been established in a number of countries and the number of accessions conserved now exceeds the six million in about 1400 genebanks (FAO 1998). The mission of the Consultative Group on International Agricultural Research (CGIAR) is to achieve sustainable food security and reduce poverty in developing countries through research and development in the fields of agriculture, forestry, fisheries, policy, and environment. Exploration, exchange, and conservation of plant genetic resources are one of the main objectives of the CGIAR. The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT – one of the 15 CGIAR centers) has responded to this need by establishing a Genetic Resources Unit for assembly, characterization, evaluation, maintenance, conservation, documentation and distribution of germplasm of sorghum (*Sorghum bicolor* (L.) Moench.), pearl millet (*Pennisetum glacum* (L.) R. Br.), chickpea (*Cicer arietinum* L.), pigeonpea (*Cajanus cajan* (L.) Millsp.), groundnut (*Arachis hypogaea* L.), finger millet (*Eleusine coracana* (L.) Gaertn.), foxtail millet (*Setaria italica* (L.) P. Beauv.), barnyard millet (*Echinocloa crus-galli* (L.) P. Beauv.), kodo millet (*Paspalum scrobiculatum* L.), little millet (*Panicum sumatrense* Roth. *ex* Roem. & Schult.), and proso millet (*Panicum miliaceum L.*).

Genetic variation, once considered unlimited, is fast eroding as modern cultivars replace traditional cultivars over large areas and natural habitats of wild relatives of cultivated species are destroyed. Several landraces now conserved in the ICRISAT genebank have disappeared from their natural habitats in Africa and Asia. Genetic variation must be conserved and effectively utilized to combat new pests and diseases, and to produce better adapted varieties for the changing environments. Seed conservation has vital role in preservation of genetic variability as it is simple to handle, cost-effective and capability of maintaining genetic stability over long time periods. Seed conservation is a popular tool for

germplasm conservation at the global level. The most important components of managing *ex situ* germplasm include well established procedures for collection/assembly, characterization, conservation and sound scientific approaches for effective utilization of conserved germplasm.

Germplasm assembly at the ICRISAT

When ICRISAT was established in 1972, efforts were made to assemble the germplasm of mandate crops that existed with various research institutes in India and other countries. The Rockefeller Foundation had assembled over 16,000 sorghum germplasm accessions from major sorghum areas, and ICRISAT acquired 11,961 accessions of collections in 1974 that existed in India and USA. ICRISAT also obtained 2000 accessions of pearl millet collected by the Institut Francais de Recherché Scientifique pour le Développement en Coopération (formerly Office de la Recherché Scientifique et Technique d 'Outremer (ORSTOM) in Francophone, West Africa.

The germplasm of chickpea and pigeonpea originally collected and assembled by the former Regional Pulse Improvement Project (RPIP), a joint project of the Indian Agricultural Research Institute (IARI), New Delhi; the United States Department of Agriculture (USDA); and Karaj Agricultural University in Iran, formed the initial collection. Sets of this germplasm, which were available in several agricultural research institutes in India and Iran, and at the USDA, were donated to ICRISAT in 1973. ICRISAT also acquired over 1,200 chickpea accessions from the Arid Lands Agricultural Development (ALAD) program in Lebanon. Similarly, much of the groundnut germplasm was received from the Indian groundnut research program, [now the National Research Center for Groundnut (NRCG), Junagadh], and USDA. Besides germplasm donations by the All India Coordinated Research Projects on various crops, considerable number of germplasm were received from agricultural universities at Pantnagar (Uttarakhand), Rajendranagar (Andhra Pradesh), Ludhiana (Punjab), Coimbatore (Tamil Nadu), Jabalpur (Madhya Pradesh), Rahuri (Maharashtra) and IARI at New Delhi. Recently, in 2004~05, we obtained chickpea germplasm samples from Washington State University, Pullman, USA (2083 cultivated, 68 wild) and ICARDA, Syria (682 cultivated, 21 wild). Over 400 accessions each of sorghum and pearl millet collected in Niger, about 200 samples of pigeonpea collected from Mozambique, Tanzania and Uganda were received from our regional genebanks in Niamey and Nairobi.

Assembly of cultivars and elite germplasm from research organizations

The National Research programs in most countries, Agricultural Universities, Regional Research Organizations and the International Agricultural Research Centers are engaged in developing crop cultivars/elite breeding lines. These germplasm lines are also conserved in ICRISAT genebank for future utilization.

Germplasm collections through explorations

The fundamental objective of collecting plant genetic resources is to capture the maximum amount of genetic variation in the smallest number of samples (Marshall and Brown 1975). The development of efficient strategies depends on the extent of the information on the type of genetic variation in target taxa populations and their distribution in the target geographical region (Allard 1970). However, when information is lacking on the target species and the collecting area it might be prudent to organize an exploration mission to collect such information. In collaboration with national programs, ICRISAT scientists conducted over 200 expeditions to collect several landraces on the verge of extinction, braving difficult terrain, hostile environments, and harsh conditions. Details on collected samples are recorded in the germplasm collection data sheet (Appendix 1) (p.62). The existing collections represent 70%~80% of the available diversity, there is continuing need to rescue endangered germplasm. Analyses of diversity in the existing collections using GIS tools facilitate identification of gaps to launch targeted collections. Germplasm collecting is expensive. Therefore, we should review the past collections of the crop before embarking on a new collection trip. If others have already explored the area under consideration, we should try to secure the germplasm from them. In some crops, for example in pearl millet, which is a highly cross-pollinated crop, the early collections may have lost their genetic identity because of poor maintenance. Hence, Harlan (1973) suggested fresh systematic collecting in such cases.

Germplasm collection at ICRISAT

The Rajendra S Paroda Genebank, ICRISAT, Patancheru, India conserving 118,882 accessions of the five mandate crops and six small millets from 144 countries (Table 1), represents one of the largest collections in the CGIAR system sharing the institute's mission to achieve global food security. The collection includes landraces (94,595), non-domesticated species (2597) advanced and old cultivars (1545) and breeding lines (17,874).

Information on coordinates of sites of collection is documented on 52,704 accessions. The collection represents both insurance against genetic erosion and a source of tolerances to diseases and pests, climatic and other environmental stresses, improved quality and yield traits for crop improvement.

Table 1. Germplasm holdings in the ICRISAT Genebank, Patancheru, India.

Crop	Active collection	Base collection	Accessions held in-trust
Sorghum	37,904	34,313	36,771
Pearl millet	21,594	20,343	21,563
Chickpea	20,140	16,977	17,124
Pigeonpea	13,632	11,794	12,389
Groundnut	15,419	12,640	14,803
Finger millet	5,949	4,620	5,949
Foxtail millet	1,535	1,054	1,535
Proso millet	842	576	835
Little millet	466	384	462
Kodo millet	658	630	656
Barnyard millet	743	487	743
Total	118,882	103,818	113,830

Germplasm collections held in-trust

The earth's natural resources are finite and vulnerable. Several countries have pledged to stem the rapid loss of biodiversity and sustain this vital resource for the present and future generations. The plant genetic diversity created in farmer's fields over the millennia and by scientific research institutions over the last century is complemented by diversity present in the wild relatives of the crop species. The collections held at the genebank have been assembled over the last three decades through donations from other genebanks, through collaborative collection expeditions with national programs, from breeders around the world and from within the crop improvement programs of the Centre. A majority of this collection (97.6%) was placed in-trust with the Food and Agriculture Organization (FAO) of the United Nations, Rome, Italy. The materials will be maintained at

international standards, and will continue to be made available to the world community with the understanding that no intellectual property protection is to be applied to the material.

Germplasm characterization

Adequate characterization for agronomic and morphological traits is necessary to facilitate the utilization of germplasm by breeders. To achieve this, germplasm accessions of all crops were sown in batches over the years and characterized for morphological and agronomic traits. Germplasm screening against biotic and abiotic stresses, and the estimations of grain food quality were conducted jointly with various disciplinary scientists. Germplasm sets were evaluated for agronomic performance over locations jointly with NARS scientists in Canada, China, Ethiopia, India, Indonesia, Japan, Kenya, Nepal, Thailand, Ukraine, USA, and Vietnam. The results of joint evaluations have led to better understanding of the germplasm material conserved at ICRISAT genebank by the NARS scientists.

The conserved germplasm has been characterized (96.3% of the collection) for important morpho-agronomic characters and germplasm seed samples distributed to bonafide researchers for utilization in crop improvement programs all over the world. The collection represents a wide range of diversity for different morpho-agronomic characters, including some important seed traits such as shape, size and texture and chemical composition. Majority of the accessions in the collection (99.7%), excepting few in groundnut, sorghum, and pearl millet, are seed producing and seeds are essentially orthodox in nature.

Germplasm characterization refers to recording of distinctly identifiable characteristics, which are heritable. This is distinct from preliminary evaluation, which is the recording of a limited number of agronomic traits important in crop improvement. Germplasm characterization is carried out in precision fields under adequate agronomic conditions and plant protection. For each accession several morpho-agronomic traits are recorded using the descriptors developed in collaboration with Bioversity International (formerly IPGRI). Following these procedures, majority of the germplasm collection at ICRISAT genebank has been characterized. Systematic description of each accession leads to classification in small and well-organized sectors that will facilitate enhanced utilization of germplasm. The major objectives of germplasm characterization are:

- To describe accessions, establish their diagnostic characteristics and identify duplicates

- To classify groups of accessions using sound criteria
- To identify accessions with desired agronomic traits and select entries for more precise evaluation
- To develop interrelationships between, or among traits and between geographic groups of cultivars
- To estimate the extent of variation in the collection

To accomplish these objectives, a multi-disciplinary approach is essential. At ICRISAT, the data generated by various disciplines are fed back to the germplasm database. As a result of intensive field and laboratory screening and purification, a wide range of sources for desirable traits were identified in the assembled germplasm.

Regeneration of germplasm

Seeds lose viability even under good storage conditions and it is necessary to regenerate accessions from time to time, the frequency of regeneration depends on the initial viability, the rate of loss of viability and the regeneration standard (i.e. the percentage viability at which it is decided to regenerate the accession) (Roberts 1984). The aim of regeneration is to increase the quantity of seed of any accession where the number of seeds available has been depleted, or to restore maximum viability to a seed lot. Regeneration of germplasm is one of the most crucial processes in genebank management. It is costly in terms of resources and time, and it involves the risk to genetic integrity of the accessions. The methods employed for regeneration vary considerably according to the crop species (Figure 1 and 2) (p.63 and p.64), and its reproductive system (inbreeding or out-breeding) (Breese 1989).

Germplasm regeneration (except pigeonpea and small millets) is mainly carried out in the post-rainy season (Nov-May) at ICRISAT, Patancheru. Due to low ambient relative humidity and absence of rains, incidences of diseases and pests are low, and consequently the quality of seed produced is high. Regeneration is carried out in precision fields and under good agronomic management for obtaining seeds of good quality and vigor. Optimum plant stand and suitable pollination control measures are required for maintaining genetic integrity in crops like sorghum, pearl millet, and pigeonpea (where out-crossing exists). Germplasm collections contain accessions originating from a wide range of environments and the site of regeneration may not be optimal for all accessions. It would be ideal to regenerate germplasm in near-optimum locations, and meet the requirements of specific cultivars.

Efficient management of seed germplasm collections therefore entails minimizing the frequency of regeneration. This can be achieved by maximizing the seed longevity. Seeds are a product of the seed production environment as well as the genetic constitution of the parent plants. The complexity of environmental conditions, including soil and climate, frequently override the expression of genetic characters. Therefore, to improve seed quality, germplasm regeneration programs should stress improved management and production practices. Several pre- and post-harvest and seed drying practices influence initial vigor and subsequent longevity of regenerated seed lots (Kameswara Rao and Sastry 1998). Wild species and critical accessions with low viability/limited seed stocks need to be multiplied in the glasshouse under adequate protection. Detailed cleaning procedures for germplasm seeds are presented in Hanson (1985). It is important that harvested germplasm material is processed as soon as possible to avoid unnecessary losses or decrease in seed longevity. Widrlechner (1998) has described various managerial decisions for germplasm regeneration.

Germplasm conservation

The conservation of germplasm in genebanks in the form of seeds requires that the integrity of the material conserved be maintained to the highest standard over prolonged periods of time. For this to happen, it is necessary to set standards based on current scientific knowledge and available technologies for the proper handling and storage seeds in genebanks that will ensure their conservation over the longest possible time, without the need for frequent costly regeneration. Standards for routine genebank operations and quality assurance were described by Dulloo and Engels (2003). Seeds are stored short-term as required for carry over seeds, or for considerably longer term as required for germplasm accessions and high value seed stocks. The full benefits of any storage system are realized only when the seeds intended for storage have high initial quality. Therefore, maximum seed quality and vigor are of paramount importance in germplasm management. Several pre- and post-harvest factors such as crop management, seed production environment, maturity, harvest and cleaning and drying practices influence initial seed quality and its subsequent longevity. Maintaining seed quality in the accessions of a large collection requires careful planning and following standard protocols during the process of seed production and storage. *Ex situ* seed storage is the most convenient and widely used method of conservation.

Types of conservation

Active collections refer to collections kept for medium-term, which are immediately available for distribution for utilization and for multiplication. Active collections are kept in conditions, which ensure that the accession viability remains above 65% for 10~20 years. Different combinations of storage temperature and moisture content can provide this longevity (IPGRI 1996). Ideally, these are maintained in sufficient quantity to be available on request. The active collections of ICRISAT genebank are stored in standard aluminum cans for all crops and in plastic cans for groundnut at 4°C and 30% relative humidity (Figure 3) (p.65). Depending on the crop species, the equilibrium moisture content for these samples ranges between 7% and 10%.

Base collections refer to collections kept for long-term, solely for 'posterity', and are not drawn upon except for viability testing and subsequent regeneration. The accessions in base collection should be distinct, and in terms of genetic integrity, as close as possible to the sample provided originally. The base collections of ICRISAT germplasm are maintained at –20°C in vacuum packed standard aluminum foil pouches at 3%~7% seed moisture content, depending on the crop species and with initial seed viability above 85%. Base collections ensure long-term viability of material (more than 50 years) as a security to the active collection. The storage conditions maintained for both the collections are the preferred standards for international genebanks. Hamilton *et al*. (2003) have described considerations for improved conservation and utilization concepts and strategies.

Safety backup

ICRISAT's agreement with FAO places the germplasm collections under the auspices of FAO, and requires safety back up for long-term conservation in countries out side India. We have initiated efforts conserving 3800 chickpea at ICARDA (Syria) and 5205 pearl millet, 2006 groundnut, and 7622 small millets (six crops) accessions at ICRISAT Regional Genebank at Niamey in Niger.

Svalbard Global Seed Vault (SGSV)

Located on the Norwegian island of Spitsbergen near the town of Longyearbyen (130 m above seas level) in the remote Arctic Svalbard Archipelago, a Seed Vault has been established to preserve unique duplicate samples of seeds held in genebanks worldwide (Figure 4) (p.65). The Seed Vault provides an insurance against the loss of seeds in

genebanks, as well as a refuge for seeds in the case of large scale regional or global crisis. Seed Vault has capacity to conserve 4.5 million seed samples, with each sample containing on average 500 seeds, a maximum of 2.25 billion seeds can be stored at –18ºC. ICRISAT has committed to place 111,000 FAO-designated germplasm of sorghum, pearl millet, chickpea, pigeonpea, and groundnut, and six small millets, in phased manner over next five years, with first batch of 20,000 accessions deposited in September in 2008.

Seed moisture content during conservation

Seed moisture content is the amount of water in the seed and is usually expressed as a percentage. Under all storage conditions, the moisture content of seeds comes to equilibrium with the relative humidity of the surrounding atmosphere. Even small changes in moisture content have a large effect on storage life of seeds. For genebank purposes, seed moisture content is usually expressed on a wet weight basis. Estimation of seed moisture content is one of the most important aspects of seed processing as several management decisions are based on seed moisture level. Methods prescribed by the International Seed Testing Association (ISTA) are used for determining the seed moisture content in the genebank – a low-constant temperature oven-drying method (103°C for 16 hours) for groundnut seeds and a high-constant temperature oven-drying method (130°C for 1~2 hours) for sorghum, millets, chickpea and pigeonpea. Estimates of moisture content of seed determine the need for drying depending on where the seed is stored. Seed moistures content for long-term conservation ranges between 3%~7% for different crops, while under medium-term conditions it is 6%~8% for groundnut and 8%~10% for other crops.

Seed drying

The longevity of seeds can be improved to a larger extent with comparatively little investment. Seed longevity depends upon crop species, the initial quality of the seed, the moisture content to which seeds have been dried and the temperature at which they were stored. Sun drying and or forced ventilation drying with heated air are generally used to reduce seed moisture content. For long-term conservation of germplasm seeds, it is recommended to dry at low temperature (15°C) and relative humidity (15%) to avoid any adverse effects of drying on the initial quality and subsequent longevity (Figure 5) (p.66) (Cromatry *et al*. 1982). Clean muslin cloth bags permitting free flow of air during drying are used in this process. Following this process, seeds of different crops with initial moisture

contents between 8.6% and 11.9% are safely dried to 3.4%~5.9% within four weeks for long-term conservation (Sastry *et al*. 2003). Ellis *et al*. (1990) recommended that the moisture content of many oil seeds could be reduced to values between 2% and 4% with considerable benefit. Ultra dry storage of oily seeds would be worth not only in refrigerated conditions but also under ambient storage conditions when funds don't allow refrigerated facilities.

Seed viability testing

The standard germination test is widely accepted and direct measure of seed viability (Figure 6) (p.67). Seedlings are evaluated and classified as normal, which are capable of developing into plants given favorable conditions and abnormal, which are incapable of further development, suffer deficiency, decay or weakness (Figure 7) (p.68). General guidelines and specific advice on the conduct of germination and appropriate dormancy breaking procedures are available in the Hand Book of Seed Technology for Genebanks (Ellis *et al*. 1985).

Seed viability monitoring

The viability of seeds stored in a genebank decrease gradually during storage and genebank accessions should be monitored regularly for viability to avoid excessive deterioration. The monitoring intervals depend on the species, viability at the beginning of storage, and the conditions of storage. A recent monitoring of the health of seed conserved for 10~25 years (MTC) indicated greater than 75% seed viability for majority of the accessions (Table 2). Accessions with declining seed viability (less than 75% seed germination) are regenerated on priority and the old stock is replaced with fresh seeds.

Germplasm documentation

Documentation is essential in good genebank management to allow efficient and effective use of germplasm. Characterization and evaluation data are of little use if they are not adequately documented and incorporated into an information system that can facilitate access to data. Information plays a significant role in biodiversity conservation. Accurate information about conserved materials is essential to enhance better use of germplasm. Computerized documentation systems enable rapid dissemination of information to users as well as assist curators manages the collections more efficiently. Tools like GIS and satellite imagery help in searching for germplasm with specific characteristics, monitor changes in

crops and varieties or deciding where to locate an *in situ* reserve. The Genebank Information Management System (GIMS) of ICRISAT is a user-friendly module designed to integrate various documentation activities, provide information on accessions due for regeneration /viability monitoring at any given point of time.

Table 2. Seed viability of active collection of cultivated germplasm conserved at ICRISAT Genebank, Patancheru, India.

Crop	No. of accessions tested	Mean viability (%)	No. of accessions in viability range	
			<75%	76%~100%
Sorghum	36,591	95.0	92	36,499
Pearl millet	20,770	93.4	167	20,603
Chickpea	16,974	96.1	73	16,901
Pigeonpea	12,786	95.0	3	12,783
Groundnut	13,489	97.7	258	13,231
Finger millet	5,010	96.2	59	4,951
Foxtail millet	1,535	87.5	195	1,340
Proso millet	833	96.2	17	816
Little millet	464	95.3	11	453
Kodo millet	658	95.1	7	651
Barnyard millet	739	93.4	56	683
Total	109,849	94.6	938	108,911

The vast germplasm data collected on chickpea and pigeonpea germplasm has been summarized and presented to users in the form of catalogs (Pundir *et al*. 1988, Remanandan *et al*. 1988). Details on germplasm exploration and collection missions were summarized as progress reports. Core collection (10% of entire collection) and mini core collection (10% of core collection or 1% of entire collection) of ICRISAT mandate crops were established and the information was published through journal articles (Greiner *et al*. 2001); Bhattacharrjee 2000; Upadhyaya and Ortiz 2001; Upadhyaya *et al*. 2001a; Upadhyaya *et al*. 2002; Upadhyaya *et al*. 2003; Upadhyaya *et al*. 2006d; Upadhyaya *et al* 2008b, Reddy *et al*. 2005) for the benefit of fellow research workers. A Manual of Genebank Operations and Procedures' has also been published (Rao and Bramel 2000) documenting the history of the collections, procedures for germplasm acquisition, maintenance, documentation, conservation, and distribution.

Germplasm distribution

Distribution of germplasm and related information is fundamental to ICRISAT's mission of increasing crop productivity and food security. As per the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) germplasm is supplied under the Standard Material Transfer Agreement (SMTA). Germplasm conserved at ICRISAT genebank has become an important source of diversity available to researchers in both public and private sectors through out the world. For example, between the years 1975 and 2008, ICRISAT genebank has distributed over 692,000 samples of its mandate crops and small millets to users in 144 countries. The global collections held at ICRISAT serve the purpose of restoration germplasm to the source countries when national collections are lost due to natural calamities, civil strife, etc. We supplied 362 sorghum accessions to Botswana; 1827 sorghum and 922 pearl millet to Cameroon; 1723 sorghum and 931 chickpea to Ethiopia; 838 sorghum and 332 pigeonpea to Kenya; 1436 and 445 sorghum accessions respectively to Nigeria and Somalia; 71 pigeonpea accessions to Sri Lanka and 44,701 accessions of ICRISAT mandate crops to the National Bureau of Plant Genetic Resources (NBPGR), India. Thus the national programs of several countries have regained their precious plant germplasm heritage which could have been lost if this was not conserved in the ICRISAT genebank.

Impact of germplasm supply

Besides distribution and restoration of native germplasm to several countries, ICRISAT genebank has promoted testing and release of several of its germplasm accessions directly as cultivars in different countries. In total 66 germplasm accessions of different crops conserved in the genebank have been released directly as cultivars in 44 countries contributing to food security. As detailed above, and a vast number of germplasm accessions distributed have been used as building blocks for hybrids that are cultivated in many parts of the world. As of December 2007, seventy seven national programs have released 548 cultivars using breeding materials supplied by ICRISAT. Few examples of ICRISAT germplasm that have contributed significantly towards food security are described here.

Pigeonpea germplasm accession ICP 8863 collected from farmer's field in India was found very promising against fusarium wilt and was purified for the trait. The purified line was

found high yielding and it was released for cultivation in 1986 as Maruthi in Karnataka state, India. This variety is also grown on large hectares in adjacent states, namely, Maharashtra and Andhra Pradesh (Bantilan and Joshi 1996). A sorghum variety, Parbhani Moti was released in Maharashtra, India, in 2002. This variety is an excellent Maldandi-type [predominant postrainy (Rabi) sorghum landrace in Maharashtra and Karnataka states of India] with large, lustrous grains and high yield. This was selected from a germplasm collection from Ghane Gaon, Sholapur district of Maharashtra, India made by ICRISAT genebank staff during 1989. Iniari is large seeded, early maturing and high tillering pearl millet landrace found in Benin, Burkina Faso, Ghana and Togo. This landrace was selected and a variety ICTP 8203 was released as MP 124 in Maharashtra and Andhra Pradesh and PCB 138 in Punjab, India in 1988. The same was released as Okashana 1 in Namibia and as Nyakhombe in Malawi. Direct selection from the same landrace lead to the development of large seeded, downy mildew resistant male sterile line ICMA 88004 (Rai 1995). Another example is the release of barnyard variety (PRJ 1) in Uttaranchal state, India during 2003. This variety yielded 45.4% higher grain yield compared to the check variety VL 29. It provides substantial fodder yield as well. This variety is a selection from ICRISAT germplasm collection IEC 542 that originated in Japan.

Utilization of germplasm in crop improvement

The increase in accession numbers in genebanks and lack of corresponding increase in their use by the crop improvement scientists was a clear indication that the collections were not being used to their full potential (Marshall, 1989). A very large gap exists between availability and actual utilization of the materials. This was true both in the International Programs (CGIAR institutes) as well as in the national programs. For example, very few of the >14, 000 groundnut and >19, 000 chickpea accessions conserved in the genebank have been utilized in cultivar development of these two crops at ICRISAT (Upadhyaya *et al*., 2003, 2006a). Similarly, in the national programs, the germplasm lines used in breeding programs are very limited. In China, the introduced germplasm and wild relatives have seldom been used in groundnut improvement. In USA, the cultivar ‘Dixie Giant’ was a germplasm source in all pedigrees of runner type groundnut and ‘Small White Spanish-1’ cultivar in >90% pedigrees. These two lines contributed nearly 50% of the germplasm of runner cultivars of groundnut in the USA. In India, 86 chickpea, 14 lentil, and 47 pigeonpea varieties have been developed through hybridization between 1967 and 2003. Only 10 germplasm lines contributed 35% of genetic base in chickpea, 30% in lentil, 48% in pigeonpea, 69% in

urdbean, and 71% in mungbean. Most plant breeders prefer to work with their own breeding lines, rather than exotic materials. Not only the limited use of germplasm is a worrisome issue, the large-scale deployment of single cultivar complicates the whole situation even more. For example in the Netherlands, the three top varieties of nine major crops covered from 81% to 99% of the respective planted area. One cultivar accounted for 94% of spring barley. Sometimes, even if the number of cultivars is more, the degree of genetic diversity between them is very low. In European barley, the protection against powdery mildew is increasingly dependent on one gene and one fungicide. Extensive use of fewer and closely related parents in crop improvement is contrary to the purpose of collecting large number of germplasm accessions, and could result in vulnerability of cultivars to pests and diseases. The fears of epidemics similar to the southern corn leaf blight in the USA (resulting in huge economic loss) and late blight of potato (that wiped out the potato crop resulting in the famine in Europe) due to narrow genetic base of crop cultivars looms large even today.

Developing core and mini core collections

The main reason for low use of germplasm in crop improvement programs is the lack of information on large number of accessions, particularly, for traits of economic importance which display a great deal of genotype x environment (G x E) interaction and require multilocation evaluation. To overcome the size related problem of collection, developing a “core collection”, consisting about 10% of entire collection, representing the genetic variability of the entire collection, has been proposed. In developing a core collection, available passport and characterization/evaluation data was used. Grouping of accessions from geographically similar countries, or regions of a big country, helps in making homogeneous groups. The data on accessions in the regional groups is then subjected to multivariate analysis to classify the accessions in to different clusters using a suitable clustering method. From each cluster 10% accessions are randomly selected to identify a core collection. Core and entire collections are compared for various parameters to determine whether core collection is representative of entire collection. Scientists at ICRISAT have developed core collections of all mandate crops and finger millet and foxtail millet (Table 3).

However, it soon became evident that developing core collections will not solve the problem of low use of germplasm, as even the size of core collection would be unwieldy for convenient exploitation by the breeders and other crop improvement scientists. This was

particularly true in the crops where entire collection is too large (several thousands). To overcome this, Upadhyaya and Ortiz (2001) proposed “mini core collection” concept and suggested a seminal two-stage strategy in chickpea. The first stage involves developing a representative core collection (about 10%) from the entire collection using all the available information on origin, geographical distribution, and characterization and evaluation. The second stage involves evaluation of the core collection for various morphological, agronomic, and quality traits, and selecting a further subset of about 10% accessions from the core collection. Thus the mini core collection contains 10% of the core or ~1% of entire collection, and yet represents the diversity of the entire collection. At ICRISAT, mini core collections have been established for chickpea, groundnut, pigeonpea, and sorghum; and analysis is in progress to establish mini core for pearl millet and finger millet (Table 3).

Table 3. Core and mini-core collections developed at ICRISAT.

Crop	No. of accessions used	No. of traits involved	No. of accessions	Reference
		Core		
Sorghum	22,474	20	2,247	Grenier *et al*., 2001
Pearl millet	16,063	11	1,600	Bhattacharjee *et al*., 2007
Pearl millet (augmented)	20,844	12	2,094	Upadhyaya *et al*., 2008b
Chickpea	16,991	13	1,956	Upadhyaya *et al*., 2001a
Pigeonpea	12,153	14	1,290	Reddy *et al*., 2005
Groundnut	14,310	14	1,704	Upadhyaya *et al*., 2003
Groundnut for Asia	4,738	15	504	Upadhyaya *et al*., 2001b
Finger millet	5,940	14	622	Upadhyaya *et al*., 2006b
Foxtail millet	1,474	23	155	
		Mini core		
Sorghum	2,247	21	242	
Pearl millet	2,094	18	238	
Chickpea	1,956	16	211	Upadhyaya & Ortiz, 2001
Pigeonpea	1,290	16	146	Upadhyaya *et al*., 2006d
Groundnut	1,704	34	184	Upadhyaya *et al*., 2002
Groundnut Asia region	504	30	60	
Finger millet	622	20		

Using core and mini core collections to identify trait-specific germplasm for use

Due to its greatly reduced size, mini core collections provide an easy access to the germplasm collections. Breeders and other crop improvement scientists can evaluate the mini core collection easily and economically for traits of economic importance to identify trait-specific germplasm for use. The global core and mini core collections were evaluated for various biotic and abiotic stresses and for agronomic traits and the following new sources were identified for utilization.

Chickpea

- 28 early maturing accessions with an average 22.8% more seed yield than control cultivars over 5 environments (Upadhyaya *et al*., 2007b)
- 39 high grain yield accessions (desi 19; kabuli 15, and intermediate 5) based on superior performance in 10 countries (Upadhyaya *et al*., 2007a)
- 16 large seed sized kabuli type accessions
- 12 salinity tolerance accessions (Serraj *et al*., 2004, Vadez *et al* 2007)
- 18 accessions for drought related traits (Kashiwagi *et al*., 2005)
- 5 accessions for high temperature tolerance
- 67 accessions resistant to wilt; 6 resistant to dry root rot; 3 tolerant to ascochyta blight; 55 tolerant to Botrytis gray mold disease and 18 accessions for multiple resistance (Pande *et al*., 2006)
- 5 accessions tolerant to *Helicoverpa* pod borer

Groundnut

- 21 early maturity accessions similar to controls and 12.6% more yield at 75 days and 8.4% more yield at 90 days after sowing (Upadhyaya *et al*., 2006c)
- 60 accessions (*fastigiata* 15; *vulgaris* 20; and *hypogaea* 25) agronomically superior and genetically diverse for high yield, large seed size, and high shelling percentage over six environments in India (Upadhyaya *et al*., 2005)
- 158 accessions with wide range of geographic and genetic diversity for low temperature tolerance and excellent combination of pod-yield, shelling percentage, 100-seed weight, and oil and protein content (Upadhyaya *et al*., 2008c)

- 12 accessions tolerant to salinity with agronomic traits
- 18 accessions genetically diverse and agronomically similar or superior the control cultivars for drought related traits (Figure 8, Upadhyaya 2005) (p.69)
- five accessions resistant to aflatoxin

Pigeonpea

- 53 genetically diverse accessions for high yield, large seed size high harvest index
- 20 genetically diverse accessions for early maturity
- 16 genetically diverse and agronomically similar or superior the control cultivars accessions for salinity tolerance (Srivastava *et al*., 2006)
- 28 accessions resistant to sterility mosaic; 8 accessions for fusarium wilt; 78 accessions for phytophthora blight and 2 accessions for multiple diseases resistance
- 10 accessions for harvest index and 20 accessions for shelling percentage

Small millets

- 25 accessions of finger millet for high yield, large seed size and early maturity
- 25 accessions of foxtail millet for high yield, large seed size and early maturity

Utilization of mini core collections by national programs

Mini core collections of groundnut, chickpea and pigeonpea are becoming popular with the national programs scientists to identify trait-specific germplasm for use in breeding programs. Eighty one sets of mini core of chickpea, groundnut and pigeonpea have been sent to NARS in Canada, China, India, Japan, Malawi, Mexico Nigeria, Thailand, UAE, USA and Vietnam for evaluation. Scientists have identified several the following useful sources of different traits for use in crop improvement programs:

Groundnut: High oleic/linoleic acid ratio: 4 accessions (China); high oil content: 7 accessions (China); large seed size: 5 accessions (each in China and Thailand); high shelling percentage: 5 accessions (each in China, Thailand, and Vietnam); resistant to bacterial wilt: 14 accessions (China).

Chickpea: Large seeded kabuli: 13 accessions (Kanpur, India); high yield: 16 accessions and early maturity: 23 accessions (Ludhiana, India)

Finger millet: Seed yield: two accessions; fodder yield: seven; early maturity: two; basal tillers: one; and inflorescence length and width: seven (Akola, India)

Molecular characterization of germplasm collection

The revolution in molecular biology, bioinformatics, and information technology has provided the scientific community with tremendous opportunities for solving some of the world's most serious agricultural and food security issues. The Generation Challenge Program (GCP) on "Unlocking Genetic Diversity in Crops for the Resource-Poor (*www.generationcp.org)*" is helping in molecular characterization of core and mini core collections to discern the diversity at DNA level and identify genetically diverse parents for mapping and use in breeding programs.

Core or mini core collections of chickpea, groundnut, pigeonpea, sorghum, pearl millet, finger millet and foxtail millet have been genotyped as part of the composite collections under the GCP. These include chickpea**:** 3000 accessions, 50 SSR markers; sorghum**:** 3000 accessions, 41 SSR markers; groundnut**:** 1000 accessions, 21 SSR markers; pigeonpea**:** 1000 accessions, 20 SSR markers; pearl millet**:** 1000 accessions, 20 SSR markers; finger millet**:** 1000 accessions, 20 SSR markers; and foxtail millet**:** 500 accessions, 20 SSR markers. Tree diagrams of genotyping composite sets of chickpea, groundnut and pigeonpea are presented in Figure 9 (p.70). Analysis of genotyping data revealed population structure in these crops and diversity among the lines identified for a particular trait in the core or mini core collection and in the establishment of reference sets. This helped us to clarify the reasons for low polymorphism in the mapping populations made on phenotypic data beside providing breeders with the avenue of using genetically diverse parents to enhance trait (s) and developing broad based cultivars.

Molecular characterization of 2915 chickpea accessions using 48 SSR markers resulted in allele information on rare and unique alleles for seed types (desi, kabuli, pea-shaped), wild species and accessions of geographic origin – Africa, West Asia, South and South Asia, South America, North America, Europe, Oceania, Mediterranean and CIS (Table 4 and 5). The gene diversity in chickpea composite collection was 0.869. The gene diversity was similar in desi and kabuli types, low in pea-shaped and wild accessions. The range of gene diversity was more in kabuli types than desi types and gene diversity was maximum in the accessions from West Asia and minimum from Oceania.

Table 4. Allele information on chickpea composite set based on seed types.

Seed type	No. of accessions	Allele information				
		Total	Range	Mean	Rare (p=0.01)	Unique
Desi	1668	1481	9~63	31	781	297
Kabuli	1167	1288	7~52	27	691	104
Pea-shaped	70	670	4~29	14	7	4
Wild species	10	341	1~10	7	0	69
Composite collection	2915	1683	14~67	35	935	-

Table 5. Allele information on chickpea composite set based on geographical region of chickpea.

Regions	No. of accessions	Allele information				
		Total	Range	Mean	Rare (p=0.01)	Unique
Africa	150	832	4~34	17	199	10
West Asia	720	1318	8~60	27	535	114
South & Southeast Asia	1138	1322	9~61	28	678	117
South America	49	524	3~23	11	0	3
North America	94	719	3~32	15	0	6
Europe	65	647	4~24	13	5	2
Oceania	2	88	1~3	2	0	0
Mediterranean	619	1241	9~48	26	573	114
Common wealth of Independent States (CIS)	44	557	3~21	12	0	1
Composite collection	2915	1683	14~67	35	935	-

Using molecular characterization of 852 of groundnut accessions using 21 SSR markers, we secured allele information on rare and unique alleles for hypogaea, and fastigiata cultivar groups and wild species accessions and accessions of geographic origin – Africa, America, Asia, Europe and Oceania. The gene diversity in groundnut composite collection was 0.819. Wild relatives were more diverse than sub-species hypogaea and fastigiata. Groundnut accessions from Americas were more diverse followed by Asia and the gene diversity was minimum in germplasm accessions from Oceania.

In pigeonpea, molecular characterization of 952 accessions using 20 SSR markers, we assembled information on rare and common alleles for accessions representing wild and cultivated types and accessions of different geographic origins **–** Africa, Americas, Asia (six groups), Caribbean and Europe. We identified 60 alleles specific to wild and 64 alleles specific to cultivated types and wild types shared 73 alleles with cultivated type. Thirty two alleles are specific to Asia 4 (India: Andhra Pradesh, Orissa, Karnataka, Kerala and Maharashtra) and two to Africa. Asia 3 (India: Daman and Diu, Gujarat, Madhya Pradesh and Maharashtra) shared 6 alleles with Asia 4 and Asia 4 shared 5 alleles with Asia 6 (Indonesia, Philippines, and Thailand).

Molecular characterization of finger millet composite collection using 959 accessions and 20 SSR markers revealed a total of 231 alleles (110 rare and 121 common) with an average 11.5 alleles per locus. The number of alleles observed was 42 in Africana, 80 in Spontanea, 148 in Compacta, 130 in Elongata, 160 in Plana, and 206 in Vulgaris types. Thirty seven alleles were specific to Vulgaris, 5 to Plana, and 4 to Africana and 2 to Compacta. Plana and Vulgaris shared 26 unique alleles. East Africa had 29 unique alleles, South Asia had 12, and Southern Africa had 11 unique alleles. In foxtail millet, molecular characterization of composite collection using 452 accessions and 19 SSR markers revealed rich allelic diversity (362 alleles, 19 alleles per locos, 196 common alleles and 166 rare alleles), group specific unique alleles and common alleles sharing between the races and geographical groups.

The composite collections of chickpea and groundnut were also field evaluated for various qualitative and quantitative traits at ICRISAT center, Patancheru, India. Reference sets based on SSRs, qualitative traits, quantitative traits and various combinations of SSR, qualitative and quantitative traits were compared in chickpea. A SSR based reference set of 300 accessions captured 78% alleles (1315) of the 1683 alleles in composite collection (Upadhyaya *et al* 2008a). The reference set based on 7 qualitative traits captured 73.5%

alleles (1237) while SSR and qualitative trait based reference set captured 80.5% alleles (1354). This demonstrated that 7 qualitative traits were as efficient as SSRs in chickpea (Upadhyaya *et al* 2008a). Similarly, in groundnut a reference set based on 21 SSRs captured 95.1% (466) 490 alleles of composite collection. The reference set based on 14 qualitative traits captured 93.3% (457) alleles while the SSR and qualitative trait based reference set captured 95.1 % alleles (466).

We have established reference sets of 300 accessions each in chickpea, groundnut, pigeonpea and finger millet, 384 accessions in sorghum and 200 accessions in foxtail millet. The chickpea and groundnut reference sets are being phenotyped for seed yield and related traits, drought and salinity and various biotic and abiotic stresses both in the field and controlled environmental conditions. The chickpea reference set is being genotyped for an additional 100 SSR markers to study trait-marker association.

Conclusions

The Global Plan of Action (GPA) for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture (PGRFA) endorsed by the Conference of the Parties to the Convention on Biological Diversity (CBD) underscore the importance and the responsibilities for the large *ex situ* collections held by the CGIAR Centers within the frame-work of the International Treaty on Plant Genetic Resources for Food and Agriculture. ICRISAT needs to ensure that the assembled germplasm is maintained in a safe, secure and cost-effective manner and provided to all bonafide users (under SMTA) for utilization in crop improvement. The agreement between FAO and ICRISAT requires that the collections are maintained under long-term conditions, monitored regularly, and regenerated with appropriate plant population and pollination controls to ensure genetic integrity.

Germplasm is basic to crop improvement programs for sustainable agriculture. Trait-specific genetically diverse parents for genetic enhancement are the primary need of the plant breeder. Agronomically superior lines are preferred by breeders to maintain the agronomic performance of breeding lines while improving the trait. Our strategic research on core and mini core collections, and identification of new diverse sources will enhance the use of germplasm in breeding programs, aimed at producing agronomically superior cultivars with broad genetic base. Molecular characterization of mini core and trait-specific subsets will further reveal the usefulness of germplasm accessions in allele mining. Another dimension of breeders' requirements is agronomic desirability of the germplasm lines. This

helps them maintaining or even improving the agronomic performance of breeding lines while enhancing the traits expression. Thus our aim is to identify the trait-specific genetically diverse and agronomically superior germplasm lines for use in crop improvement programs to develop high yielding cultivars with a broad genetic base. The easy and convenient evaluation of mini core even for agronomic traits would help identifying such lines.

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Appendix 1

ICRISAT germplasm collection data sheet

ICRISAT — GENETIC RESOURCES UNIT—COLLECTION DATA

1. Collection number ☐ 2. ICRISAT Accession No. ☐
3. Crop species _____
4. Collector(s) _____ 5. Date _____ 19 _____
6. Country _____ 7. State _____ 8. District _____
9. Village _____ 10. Precise locality _____
11. Altitude _____ m 12. Latitude _____ 13. Longitude _____
14. Soil & topography _____
15. Precipitation: < 450 mm ☐ 451-650 mm ☐ 651-900 mm ☐ > 900 mm ☐
16. Sample source: Field ☐ Threshing Floor ☐ Store ☐ Market ☐
    Institution ☐ Other ☐
17. Local name _____ 18. Type/ Race etc: _____
19. Ethnic group _____ 20. Donor's name _____
    Donor's source: Own ☐ Local ☐ Market ☐ Others ☐
21. Cultural practices: Rainfed ☐ Irrigated ☐ Flooded ☐ Transplanted ☐
22. Planting date _____ 23. Harvesting date _____
24. Associated crop: Sole ☐ Mixed ☐ with _____
25. Population variability: Uniform ☐ Low ☐ Medium ☐ High ☐
26. Diseases _____
27. Insects _____
28. Agronomic score: Very poor ☐ Poor ☐ Average ☐ Good ☐ Very good ☐
29. Remarks: _____

Figure 1. Regeneration in cross-pollinated crops by bagging: Sorghum (top) and Pearl millet (bottom)

Figure 2. Regeneration in Pigeonpea: bagging (top), and under cages (bottom)

Figure 3. Medium-term storage facility at ICRISAT

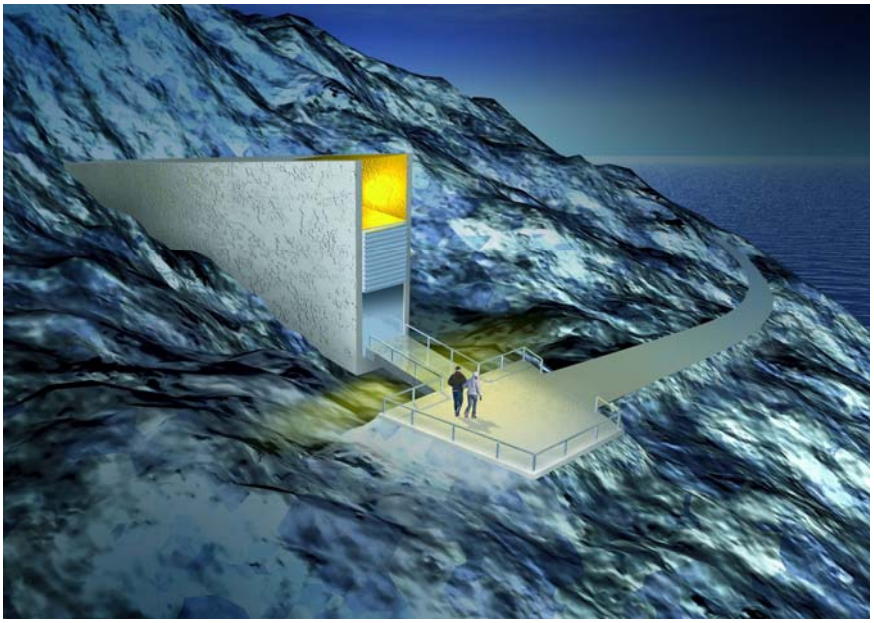

Figure 4. Svalbard Global Seed Vault, Norway for germplasm safety backup

Figure 5. Controlled environment facility for germplasm seed drying at ICRISAT

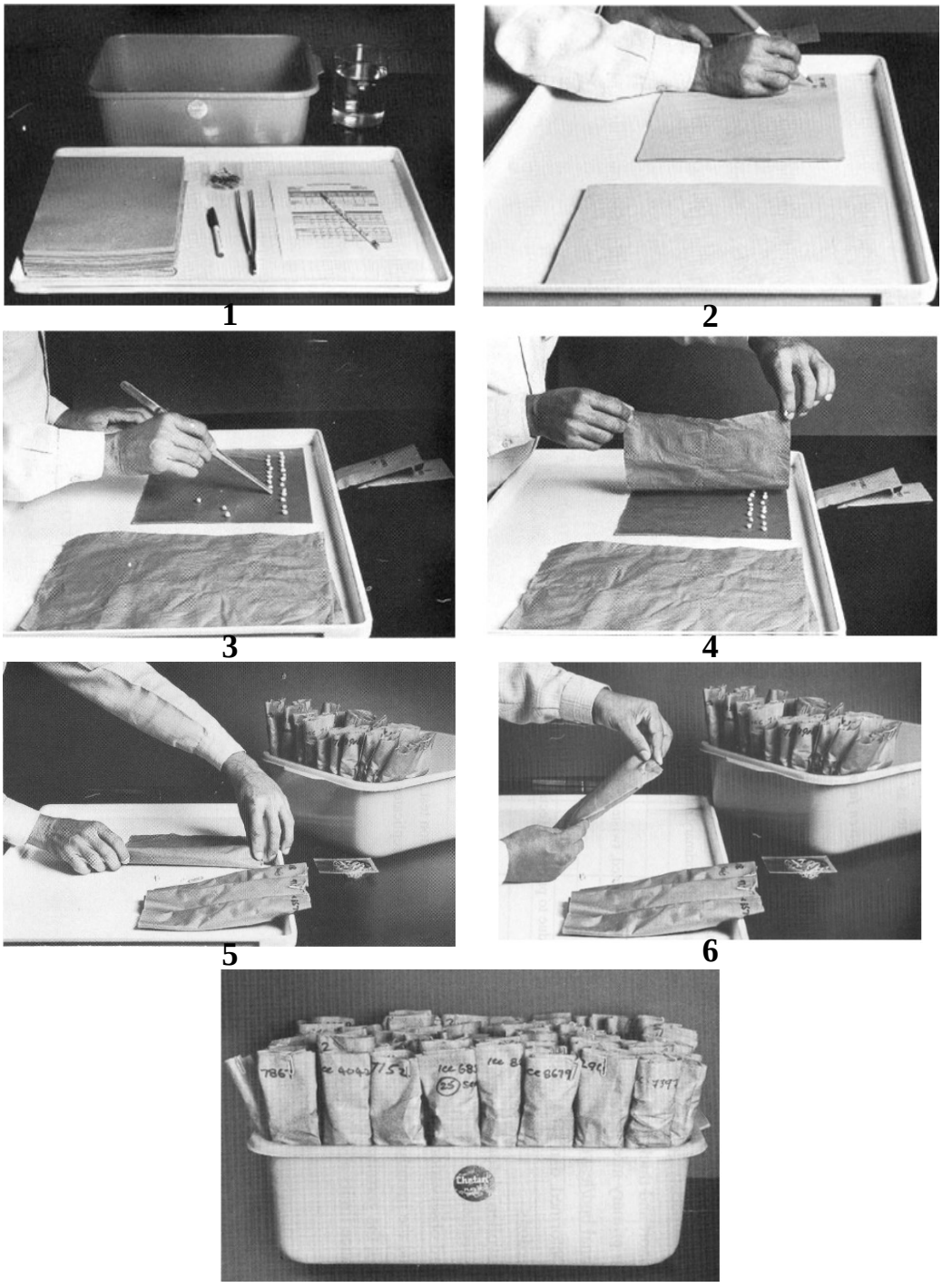

Figure 6. Testing germination of seeds using moist paper towels (1~7)

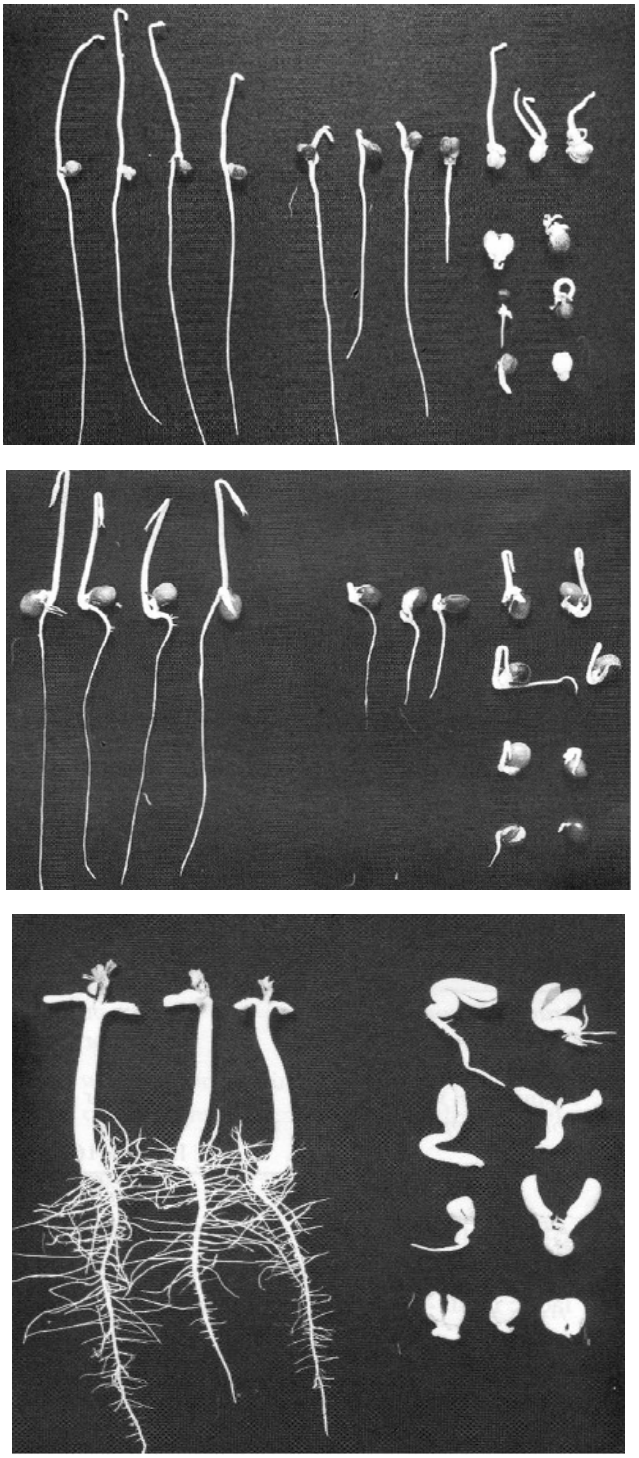

Figure 7. Seed germination test – evaluation of seedlings – normal (left) and abnormal (right) in different crops: Chickpea (top), Pigeonpea (middle), and Groundnut (bottom)

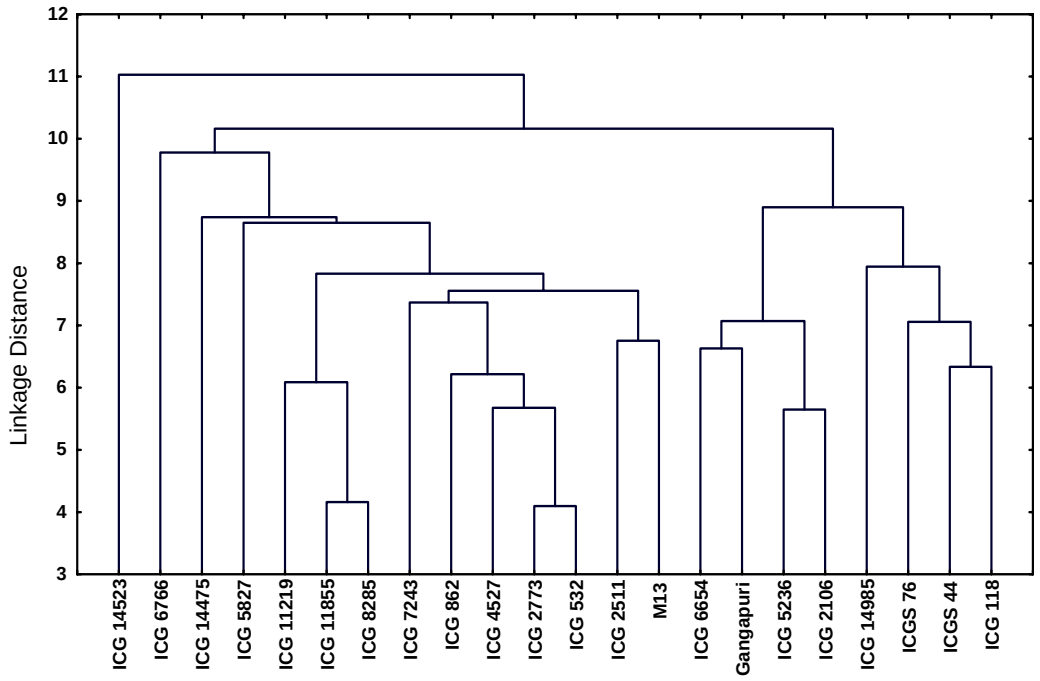

Figure 8. Dendogram based on first fifteen principal components of 18 selected groundnut accessions and four control cultivars (Upadhyaya 2005)

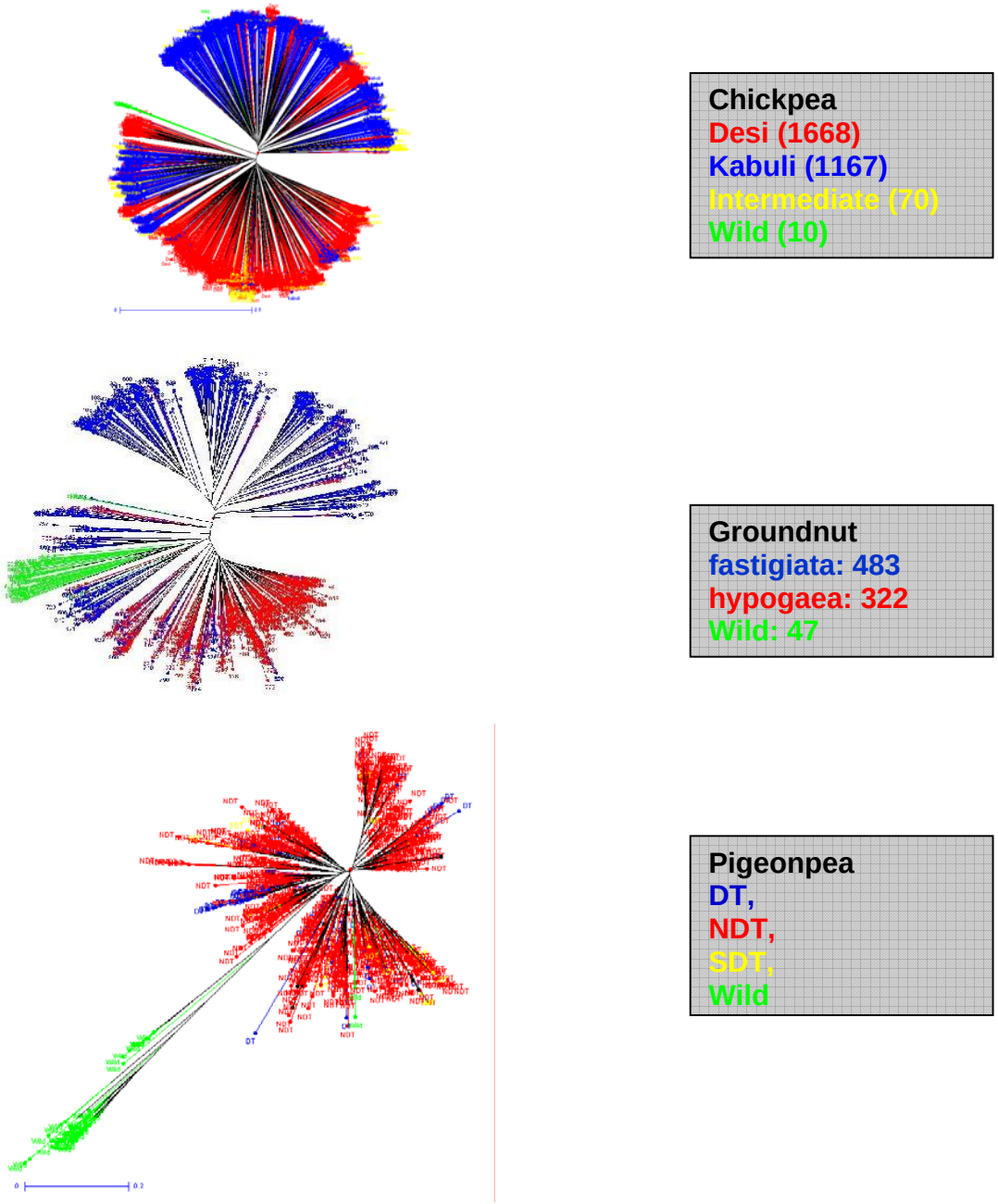

Figure 9. Tree diagrams of genotyping composite sets –
top: Chickpea (2915 accessions and 48 SSR markers);
middle: Groundnut (852 accessions and 21 SSR markers); and
bottom: Pigeonpea (952 accessions and 20 SSR markers).

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Capacity Building for Risk Management Systems on Genetic Resources
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Establishing a Taiwan Biodiversity Information Network and Its Integration with Germplasm Databanks

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Abstract

With the establishment of the “Biodiversity Promotion Plan” by the Executive Yuan, the National Science Council commissioned Academia Sinica to integrate Taiwan’s biodiversity databases. Subsequently Academia Sinica created TaiBNET in 2002 and TaiBIF in 2003. The Agricultural Research Institute’s National Plant Genetic Resources Center, which is in charge of integrating data on agriculture, forestry, fishery, animal husbandry, and germplasm, began collaborating with the Catalog of Life of TaiBNET in 2004. Through a linker, i.e., the scientific name, data in these two databases can be matched against each other. Because the TaiBIF is cooperating with GBIF, all germplasm data in Taiwan can now be accessed globally.

Introduction

Prior to 2001, biodiversity databases were established and located at different governmental and academic institutions and NGOs with no integration among them. At most, some links to certain related sites were provided. But then users had to search for the information they needed from the beginning home page. Integration work finally began in 2001, especially after the launch of the 1st five-year National Digital Archives Program (NDAP) which includes the natural heritage of specimen and species information. The “Biodiversity Promotion Plan” was also approved and executed by the Executive Yuan in the same year. That year, Taiwan joined the Global Biodiversity Information Facility (GBIF) as an Associate

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Participant so we were able to use the same metadata of the Darwin Core and DiGIR as the exchange platform to link local databases to global databases. From 2002 to 2004, The National Science Council (NSC) commissioned us to establish the Catalog of Life website (TaiBNET) with a team of more than 100 taxonomists in Taiwan. The national portal of the GBIF in Taiwan (TaiBIF) was established in 2003 under sponsorship of the NSC and the Council of Agriculture (COA). In 2007, we merged the TaiBIF into the 2nd phase of the NDAP, now called TELDAP, because international collaboration is one of the foci for this national program.

The Biodiversity Action Plan has two missions. (1) Mission D1201 – Establish biodiversity data exchange mechanisms as well as establish and integrate related databases of government agencies and institutions; and periodically add content. The executive agency is the NSC and co-execution agencies include the COA, Academia Sinica, Ministry of the Interior, Ministry of Economic Affairs, Council of Indigenous Peoples, Department of Health, Ministry of Education, Environmental Protection Administration, and Ministry of Transportation and Communications. (2) Mission D1301 – Establish national germplasm banks; and conduct research, conservation, and utilization of agriculture, forestry, fishery, animal husbandry, wildlife, and microorganism genetic resources. The COA is in charge, and co-sponsors are the NSC, Academia Sinica, Ministry of Education, and Ministry of Economic Affairs. This is also why Academia Sinica and the National Plant Genetic Resources Center (NPGRC) need to work together.

Using scientific names to integrate all biodiversity information

A correct and up-to-date biological species checklist is the most important step for integrating biodiversity databases. This is because each species has only one valid name, and the name is the only keyword or linker in all biological databases. Through the scientific name, specimen information can be accessed and queried, as can genetic data (Barcode of Life, BOL), Tree of Life (TOL), ecological distributional data, and updated species information in the Encyclopedia of Life (EOL). For work on the Catalog of Life (COL) in Taiwan, we just held a “2008 Workshop: Research and Status of Species Diversity in Taiwan” in August of this year. In November, we will publish both a hardcopy and a CD-ROM of the 1st official national species checklist. As to the BOL, Academia Sinica is a member of the Consortium of Barcode of Life organizations. In September 2007, we successfully hosted the 2nd International Barcode of Life Conference in Taipei. So far, about 300,000 barcodes for 30,000 species have

been put on the internet for public access.

As to wild animals, the Forestry Bureau of the COA is promoting a team project for collecting wildlife tissue samples for cryobanking and barcoding. Academia Sinica is in charge of establishing this database and has already accumulated about 3000 species and 8000 lots of tissue samples preserved in liquid nitrogen along with their voucher specimens. In this database, a user can learn how many species and which species have been collected by various institutions, including Academia Sinica (fishes), the Taiwan Endemic Species Research Institute, Taiwan Normal University (birds and mammals), Taipei City Zoo, NTNU (amphibians and reptiles), National Museum of Natural Sciences (invertebrates and insects), and Taiwan Livestock Research Institute (central bank).

The first 30,000 pages of species information, one species a page, of the online EOL have been made available to the public. The goal is to achieve a total of 1.8 millions pages by 2017. We would like to collaborate with the EOL in providing pages of Taiwanese endemic species from our own “Taiwan EOL”.

The TaiBIF is the national portal for the GBIF

Figure 1 shows the homepages of the Chinese and English TaiBIF website. The Life Science Department of the NSC and COA are sponsors of updating the species checklist and integrating *Digital fauna and flora*, as well as collecting data on ecological distributions; whereas NDAP funding helps integrate all contents collected from NDAP sub-projects and cross-agency integration. This website can also search for endemic species images, species information, and geographical distribution range, and link to other biodiversity databases in Taiwan, including regulations, institutions, NGOs, national parks, etc. In total, 11,775 species have been compiled in the Fauna and Flora of Taiwan in the TaiBIF. An additional 2000~3000 species are expected to be added by the end of the year.

For biodiversity-related literature, theses, symposia, research projects, and reports in Taiwan, the Science and Technology Policy Research and Information Center, National Applied Research Laboratories has collected about 31,000 records. Biodiversity-related news and activities in Taiwan are updated on a weekly basis. The website can be linked to the website of the Environmental Information Center. The geographical distribution map for each species and the specimens collected can be displayed on a GIS map by dots or 10 x 10-km grids. These data can also be exported to Google maps. Since the TaiBIF is one of the GBIF data providers, when the latitude and longitude data of these specimens are submitted to

GBIF, the locations can then be accessed on the GBIF website or other global databases such as FishBase or OBIS.

Fig. 1. TaiBIF website in Chinese and English.

TaiBNET is the catalog of life (COL) in Taiwan

To collaborate with the COL of Species 2000, we mainly use the TaiBNET website. This database generally is for integrating and updating Taiwanese native and introduced species checklists. So far, we have accumulated seven kingdoms, 51 phyla, 2614 families, and about 48,000 native species, not including introduced species. The organisms can be searched for by the classification system of kingdom phylum, class, order, and family. The statistics on the current species occurring in Taiwan in each family, order, class, and phylum are provided and are continually being updated. When a user clicks on a family, all species belonging to that particular family are listed. The species name can also be searched for using taxon names, key words, or strings. When a particular species that a user is interested in is selected, detailed information on the species is given. There are also links to other databases in Taiwan

or global databases so that further information on that particular species can be accessed.

Currently, TaiBNET has collected about 35,967 synonyms, 24,313 Chinese common names, 3417 taxonomic names, and 2953 corresponding Chinese names at the rank of family and above. Collecting synonyms is important because scientific names are often changed. Only a very few taxonomic experts know which name is valid or invalid, and users often cannot find relevant data when using old names. Since TaiBNET features synonyms, it automatically finds the correct name if a user keys in an invalid one. All data in TaiBNET are open to the public, so users, if they wish, can download data using either xml or csv format.

Many species or strains deposited at the agriculture, forestry, fisheries, and animal livestock institutes, as well as the Bioresources Collection and Research Center (BCRC) are introduced species or strains, not native species. As a result, we decided to compile lists of introduced, cultural, and naturalized species in the TaiBNET as well. Otherwise, it would not be possible to link to and retrieve the information for many non-native species. To encourage users to provide their own data, we have also prepared an interface webpage so that users can upload photos, species information, and synonyms.

Another database that the TaiBNET hosts is the experts name list, mainly for experts in taxonomy and ecology. Through this database, users can find the expert of one special taxon by choosing the expert's name, specialty, organization, or occupation as the condition of the cross search. The resulting page contains both Chinese and English information. Another advantage of having a good database is the capability to verify the correctness of the data. The TaiBNET now offers users the feature of double-checking whether the species composition or list contains spelling or typing errors, or whether the species is valid or not. By pasting the name list on the webpage of the TaiBNET, a user will receive a list of possible errors for correction. This function can significantly improve data quality.

Integration of the TaiBNET/TaiBIF with germplasm databanks in Taiwan

Figure 2 shows how we have integrated different databases from different agencies. Basically, we use the species name or the GIS distribution (GPS data) as the primary key or linker to directly access raw data or webpages of other databases. The TaiBNET and TaiBIF are the two portals for this cross-agency integration in Taiwan.

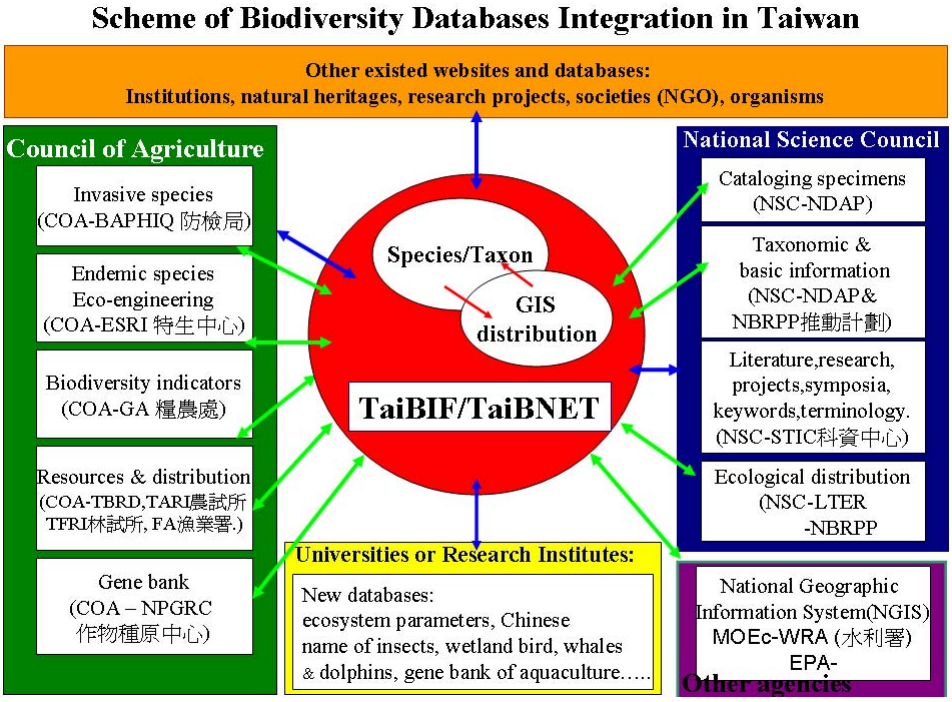

Fig. 2. Integration of databases from various agencies.

The NPGRC is in charge of coordinating germplasm databanks at various institutes of the COA. So far, the Agricultural Research Institute has collected about 1434 species which belong to 189 families and 781 genera. The total numbers of data down to strains or lines include 68,108 passport data, 27,581 records of characterization data, and 4002 images. In order to facilitate the exchange of plant germplasm information among scientists and breeders, the COA sponsored a 3-year project to integrate all germplasm data from four institutes and integrate those data with the TaiBIF and TaiBNET during 2006~2008. The first step was to compare the species lists between germplasm banks and the TaiBNET and then modify the classification system and match the species names. Table 1 shows the number of species matched up between each institute and the TaiBNET/TaiBIF, including the BCRC. Table 2 is a list of institutions and databases that have been integrated with the TaiBNET so that all information can be directly linked or mutually exchanged with each other. The BCRC, the largest and central bank for microorganisms in Taiwan, provides data on 104 species. So far, we only have a list of germplasm data from the Forestry Research Center, because they have not provided URLs of their 108 species. The Fishery Research Institute has gamete characteristics on 40 freshwater aquaculture fishes.

Table 1. No. of genera/ No. of species matching up between various institutes and the TaiBNET/TaiBIF

TaiBNET & TaiBIF include agriculture, forestry, fishery and animal husbandry information

	Genus	Species
Bioresources Collection and Research Center	53	104
Agricultural Research Institute(NPGRC)	428	675
Taiwan Forest Research Institute	77	108
Livestock Research Institute	16	21
Livestock Research Institute – Poaceae	32	52
Livestock Research Institute – Fabaceae	26	38

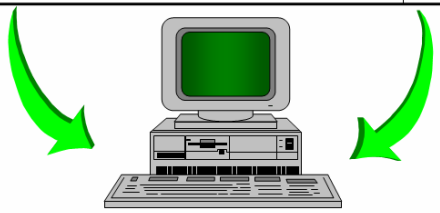

Table 2. A list of institutions and databases that have integrated with the TaiBNET

675 species at National Plant Genetic Resources Center are linked to TaiBNET through scientific names

TaiBNET 台灣物種名錄 Catalogue of Life in Taiwan

首頁 物種名錄 專家名錄 相關資料 訊息服務

本站推薦連結的網站(以學名直接與該站連結)

網站中文名稱	網站英文名稱	連結筆數
U.S. National Parasite Collections	U.S. National Parasite Collections	83
Manter Laboratory Of Parasitology	Manter Laboratory Of Parasitology	2
台灣大型甲殼類資料庫	The Large Crustacean of Taiwan	319
台灣本土植物影像資料庫	Images Database of Native Plants in Taiwan	223
台灣貝類資料庫	The Taiwan Malacofauna Database	3421
台灣魚類資料庫	The Fish Database of Taiwan	2917
台灣博物館海藻資訊網	Seaweeds Net of Taiwan	156
生物資源保存及研究中心	Bioresources Collection and Research Center (BCRC)	104
自然科學博物館自然與人文網站	The Digital Museum of Nature and Culture (National Museum of Natural Science)	1733
國立海洋生物博物館生物典藏與數位資訊網	National Museum of Marine Biology Aquarium Digital Network	596
世界魚庫 FishBase	FishBase	2917
台灣昆蟲學會	Taiwan Entomological Society	1
楊懿如的青蛙學堂	Frog School	32
台灣大蚊網站	Tipulidae in Taiwan	12
Discover Life	Discover Life	23488
農試所作物種原中心	National Plant Genetic Resources Center	675
國立台灣大學台灣植物誌電子書	Flora of Taiwan 2nd eBooks (National Taiwan University)	6
台灣原住民族生物學誌	台灣原住民族生物學誌	613

In addition to the TaiBNET, all of the germplasm data mentioned above can be searched for on the TaiBIF website as well. Due to the fact that the TaiBIF is collaborating with the GBIF, all germplasm data in Taiwan can now be accessed globally through the GBIF or any other national portal.

Future work and perspectives

Work remaining to be accomplished includes: establishing a common name list in English; increasing the number of Chinese common names; adding and linking more species names in germplasm banks; linking more webpages with information on species and lines (strains); setting up links to global germplasm data banks; and for TaiBNET, increasing the number of introduced and cultivated species included in the Catalog of Life in Taiwan.

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Capacity Building for Risk Management Systems on Genetic Resources
79~100

Enhanced Conservation and Management of Canadian Bioresources

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Abstract

An economically viable, environmentally sustainable, secure and safe agricultural system is dependent on the availability of a genetically diverse assemblage of plant, farm animal and microbial bioresources that is conserved, managed and utilized appropriately. Genetic diversity is raw material for selection and improvement in productivity and quality, resistance to pests and diseases, adaptability to changing and adverse growing conditions, materials for bio-based products, and contributes to the creation of a safe and secure food system. However, the genetic diversity of Canadian bioresources, like many others in the world is threatened by genetic erosion of crop and livestock gene pools, habitat loss, and for social and economic reasons[1]. The intent is to present various conservation and management practices which Canada has implemented to reduce the risk of genetic loss of crop and livestock gene pools with emphasis on genebanks.

Introduction

Authoritative knowledge of our bioresources, and the improvement and development of new techniques for conservation, management and utilization are ongoing challenges. The maintenance of genetic diversity requires appropriate conservation techniques, but for many species knowledge of optimal protocols is limited or unknown. The reproductive biology of many native Canadian plant species (including the wild relatives of major crops and many underutilized species) is poorly understood, making the development of regeneration procedures difficult. Conservation of fruit and potato clonal germplasm requires

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optimization of *in vitro* culture techniques, and virus indexing or heat therapy to obtain clones free of infection [2,3,4]. Knowledge of cryopreservation techniques and successful methods of regeneration for many animal/poultry species are largely lacking [5]. Understanding the molecular mechanism behind apoptosis in bull sperm may enhance survival in the female reproductive tract and increase the fertilization rate [6]. Cryopreservation of swine and avian semen has not been optimized in terms of suitable cryoprotectants, or freezing rate [7]. Vitrification, a form of cryopreservation, has not been optimized for bovine oocytes and embryos. Progress has been made in the last decade in the production of in vitro pig embryos, maturation of oocytes, fertilization, and culture including non-surgical embryo transfer, but much remains to be done [8,9,10,11]. Conservation of viral and fungal collections is challenged by a lack of knowledge of optimum storage protocols, regeneration via live hosts, the maintenance of correctly identified, pure cultures, and the development of new diagnostic tools to verify virus identities [12]. Correct identifications of both fungi and viruses are a necessity for regulatory agencies concerned with quarantine and bioterrorism issues, disease resistance studies, diagnostics research, and reference strains for indoor air quality companies, and screening programs for novel pharmaceutical compounds[13]. The characterization and evaluation of bioresource attributes enables the development of new information about, and/or identification of, new sources of plant disease resistance, improved nutritional quality and bioactive compounds. Plant germplasm with genes conferring resistance to diseases reduces the need for pesticides and contributes to environmental health [14]. A few sources of resistance to ascochyta blight in lentil and chickpea have been identified and incorporated into breeding programs, and resistant cultivars have been released. Germplasm with different sources of resistance needs to be acquired and combined to provide resistance against highly variable pathogens [15,16]. Additionally, resistant germplasm is required for cultivars where no resistance is available, or where resistance is at risk of breaking down. Many plant species native to Canada are related to crop plants, and a significantly greater proportion may have economic value [17,18,19]. Native species are sources of secondary metabolites with biological activity which may lead to new herbal, pharmaceutical or insecticidal products [20,21,22]. Compounds derived from underutilized crucifer crops such as *Camelina* and *Crambe* have wide applicability for both industrial and food uses. Wild crucifers are also a novel source of important traits for canola; eg. cytoplasmic and nuclear male-sterility inducing systems critical for the F_1 hybrid seed industry, drought tolerance, and disease and insect resistance[23,24]. Applications of molecular markers in the management of genetic resources have been successfully made to assess

the extent and distribution of genetic diversity and to evaluate genetic relationships of genebank accessions[25,26]. These applications have helped resolve issues such as accession identification and duplication [27]. Molecular diversity investigations of rare or endangered native plant species are few. Knowledge of the genetic diversity and structure, mating system and gene flow of native species is essential for monitoring their genetic status in natural populations and for the development of effective *in situ* conservation strategies [28]. The Germplasm Resources Information Network-Canada (GRIN-CA) was created to manage the information generated in the Canadian germplasm network. The challenges for future GRIN-CA development will be to maintain good communication between system developers and users, to keep the system flexible and adaptable to change, and to follow international standards. ORACLE system software is complex but flexible, and requires a considerable amount of system management, upgrading, administration and monitoring. Ongoing acquisition, storage and regeneration of germplasm including barley, oat, wheat, oilseed and pulse crops are strategically important for Canada [29,30,31,32]. Not a single major domesticated crop has either its centre of origin or domestication in Canada, and crop development will continue to depend on introduction of foreign and other diverse germplasm. Similarly, the maintenance and use of genetic diversity in Canadian farm animals requires ongoing acquisition and proper evaluations of genetic diversity within and among breeds [33,34,35,36,37].

Mandate

The mandate for the Canadian Genetic Resources Program is to conserve, preserve, enhance and increase utilization of plants, animals, microbes and plant viruses of economic importance to Canada. This mandate includes wild species including native Canadian plant species of economic importance to Canada. This mandate probably differs little from that of most other national genetic resource programs in the world. Canada's national program constantly keeps in mind methods and policies to reduce risk to collections, facilities and training to enhance capacity and what clients of the program require from it: quality germplasm for breeding and research and relevant information about the germplasm and about the genetic diversity within the bioresource.

Facilities

Adequate facilities (buildings and field plots) play a key role in the conservation of genetic resources. Facilities impact many of the basic functions conducted while maintaining

and conducting research on the germplasm conserved, in reducing risk to collections and in building national and international capacity. Security of collections is of national importance and can also play a significant role in health and safety for staff. Canada has implemented a number of security measures to ensure the safety of the facilities, the collections and for staff. Some of these are:

1. use of active and passive methods (boulders, trees, external lights) to reduce physical harm to buildings;
2. use of restricted access to buildings and seed storage vaults;
3. secure fencing around all field plots with restricted access to plot areas;
4. use of cameras at all entrances, within seed storage vaults and cryogenic rooms;
5. internal fire suppression systems (not water, but compounds (FM-200) which displace oxygen) especially in the seed storage vaults;
6. “hot buttons” which when pushed announce a major problem and call for assistance within the building and local security forces in seed storage vaults and cryogenic rooms; and
7. oxygen monitors and air replacement in cryogenic rooms, slight negative pressure.

Acquisition

Genetically diverse collections are the foundation for any national program and take considerable time, effort and planning to accumulate so as to constantly meet current and future national needs. The needs of a country will vary over time and may be domestically or internationally focused. In Canada initial plant acquisitions focused on a few important genera: *Medicago, Lycopersicum*, *Triticum*, *Avena*, *Hordeum*. Additions to collections occurred through extensive expeditions to the Mediterranean region and through exchange with other countries. Policy agreements with international agencies (ICPBR) influenced the Canadian collection and resulted in Canada accepting world responsibility for base collections of *Hordeum* and *Avena* and duplicate back up collections of Crucifers and *Pennisetum*. At one time acquisition criteria for each major crop group were established, but these proved to be too inclusive and failed to work (too little was excluded). Recently, the plant germplasm program is focusing on new acquisitions to address specific crop production concerns such as climate change (germplasm with specific stress traits (heat/drought tolerance, disease resistance) and native Canadian plants from costal areas (flooding) or high altitudes, bioproduct traits, newly registered Canadian germplasm (cultivars), and germplasm to increase the genetic diversity (genes/locations) of economic

importance including Canadian species at risk. Applying GIS technologies to identify gaps in collections, to understand the ecogeographic distribution of germplasm and to link these variables to observed genetic variation (using molecular techniques) should now be emphasized. The technologies may help us to better understand why the variation exists. The Canadian animal program is focused on acquiring only semen, embryos and suitable DNA samples (eg. blood, hair) of domestic breeds including the more than 100 breeds at risk in Canada. Samples from animals entering domestication (buffalo, elk, and deer) are also being acquired when available. Accessions in the animal program use a specific donor agreement outlining obligations including passport information.

Maintenance

Germplasm (seed) is ideally maintained in either mid-term storage (working collection) at +4°C and 20% RH or in long-term storage (base collection) at –20°C. A backup electrical generator and compressors exist for cold storage rooms. Clonal germplasm (potato, fruit tree and small fruits) is maintained in orchards, screenhouses, greenhouses or *in vitro*. Animal, microbial and virus germplasm is keep in cryogenic facilities in liquid nitrogen at –196°C or some fungi are kept as dry spores. Considerable effort has been extended to reduce risk to collections including the following: for seed, safe secure duplicate backup of samples at remote locations from Saskatoon, either with the USDA National Genetic Resources Unit, Fort Collins, CO or the Svalbard Global Crop Diversity Trust seed vault, Norway; for clonal material from within Canada backup takes place at Saskatoon, when possible. To reduce risk of loss, many clonal genebanks seek alternatives to duplicate local orchard plantings for backing-up their collections, eg., via developing cryopreservation or *in vitro* maintenance or by establishing duplicate orchard plantings at other sites. Unfortunately research for developing techniques for conserving clonal crops from seed appear lacking. Although this approach may not be feasible or biologically sound (recalcitrant versus orthodox seeds, genetic integrity issues) for some crops, it may be possible for other species or populations.

Regeneration with emphasis on cross-pollinated crops

Reasons for regeneration include: 1. low number of seeds due to: frequent request of a sample (distribution requirement); a sample entering the collection with an initial low number of seeds; the need to multiply seed stocks to meet recommended quantities for base collections; or the seeds have been identified as forming a minor part of another accession

and have to be treated separately. 2. Reduced viability due to natural aging during storage or to low quality of the original seeds. Even under optimal *ex situ* storage conditions, viability declines and the result is a loss of both genes and genotypes. In the case of unique material, such losses may be irreplaceable. Therefore, the monitoring of viability and timely regeneration must be a priority activity for any genebank to reduce risk of genetic erosion. In general, a viability of 85% is considered the minimum to avoid genetic erosion within an accession [1].

Cross-pollinated species appear to have little effect on the world's food supply – possibly no more than 1%. Important foods such as grains, potato, sweet potato, cassava, banana and coconut tend to be wind pollinated, self-pollinated, and partially insect-pollinated or are propagated asexually or develop parthenocarpically. However, when total animal and plant products are considered, about 1/3 of the human food diet is dependent, directly or indirectly, on insect-pollinated plants. Animal food products such as beef, pork, poultry, lamb, milk and cheese contribute about half of the diet. These products are derived, in part, from insect-pollinated legumes such as alfalfa, clover, or trefoil. More than half of the world's diet of fats and oils come from oilseeds- canola, coconut, cotton, oil palm, olive, peanut, soybean and sunflower [38]. Many of these plants depend on or benefit from insect pollination. Regenerating cross-pollinated crop species is particularly challenging in gene banks for a number of reasons.

Lack of information

General patterns of pollen transfer within and between flowers and plants are well known [39,40]. Terms such as cleistogamy, autogamy (selfing), allogamy, xenogamy (crossing) illustrate the diverse array of methods plants manipulate breeding systems and control genetic structure of populations and patterns of evolution. Breeding systems are under genetic control and can be selected for. They are rarely fixed and static, but are fluid and respond to selection pressures in a variety of subtle and interrelated ways. As breeding systems control genetic variability, and are themselves controlled by components of genetic variability, they are subject to feedback positive, negative or stabilizing [39]. Part of the challenge is that most seed plants have a wide range of reproductive options available for selection. These may arise constantly, through genetic variation, or intermittently, through mutation. Broadly speaking these are [39]: hermaphroditic versus unisexual; self-pollination

versus cross-pollination; self-fertilization versus cross-fertilization; and sexuality versus asexuality.

Detailed pollination requirements for the major cultivated crop species are known [41,42,39,43]. However, the reproductive biology for many crop species (including wild relatives of major crops, underutilized or minor crops) is not yet sufficiently understood, making the development of regeneration protocols difficult and placing them at risk to genetic erosion. This matter requires urgent research.

Comparative studies among species within a genus provide valuable insights into the variability of reproductive systems. Estimates of the amount of self- or cross-pollination and self-incompatibility can be determined using 8 treatments involving bagged or unbagged and emasculated or untreated flowers [40]. The rate of self-pollination can be estimated by comparison of the values of seeds from naturally pollinated flowers with those of hand self-pollinated and hand cross-pollinated. The selfing rate, S can be estimated following Charlesworth and Charlesworth [44]:

$$S = \frac{P_x - P_o}{P_x - P_s}$$

where P_x is the value from crossing, P_s for selfing, P_o for the open-pollination. Similarly a measure of self incompatibility can be determined [45]:

$$\text{Self incompatibility} = \frac{\text{seed set from self-pollination}}{\text{seed set from cross-pollination}}$$

Caution should be employed as self compatibility levels may vary between individuals of the same species and among species [46]. Estimates of the level of cross-pollination can also be determined. The ratio between the number of pollen grains and ovules (the P:O ratio) reflects the breeding system [47]. The out-crossing level of a given species shows a high relationship to the breeding system, the floral size, the temporary separation of anther dehiscence and stigma receptivity, and the spatial relationship of the stigma and the anther [47], although deviations from the P:O ratio standards are now being documented [40].

Concerns about genetic erosion and drift during regeneration

Genetic erosion is the loss of genetic diversity, including the loss of individual genes or particular combinations of genes such as those expressed in landraces. The term “genetic

erosion" is sometimes used in a broad sense, referring to the loss of populations, varieties, or species or more narrowly as the loss of a gene or allele.

Populations are maintained in their natural habitats in unstable equilibrium through the pressures of natural selection. These pressures cannot be emulated during *ex situ* regeneration, and may be replaced by opposing directional pressures, thus leading to accelerated loss of adaptive characteristics. Natural selection depends on the total fitness of individual phenotypes and may operate through: 1) differential survival, and 2) differential fecundity. Both aspects may result in gene loss or a change of gene frequency and a consequent change in mean performance of the population.

The rate of change for any particular trait can be most easily expressed as differential survival [48]. Change will be most rapid where there is genetic variation in highly heritable characters like resistance to disease and pests and some forms of tolerance to environmental stress; least for production characters with low heritability. The intensity of selection and heritability change over environments as a result of genotype by environment (G x E) interactions [49,48,50].

The practical approach during regeneration is to choose environments and cultural practices which reduce the selection pressures. This means ensuring all plants survive and produce seed. However, even when growth and the full reproductive cycle are obtained, natural selection can still operate through changes in the relative reproductive capacities of genotypes in different environments. Although less obvious and dramatic than differential survival, such G x E interactions affecting seed yield are likely to be a major cause of shift in populations during *ex situ* regeneration.

Risk of genetic drift due to sampling errors and genetic shift due to selection may be compounded over regeneration cycles. Frequent multiplication of an accession is another problem, particularly when the sub-sample of seed is too small to be representative of the genetic diversity of the whole accession. Many landraces are heterogeneous mixtures of genotypes, and the problems of genetic drift and shift may be greater. The factors that could cause genetic erosion and drift during regeneration have been summarized [51]. Efficient management of germplasm during regeneration (in the planting, harvesting, threshing, drying and packaging stages) can reduce the risks associated with genetic erosion and drift.

The necessity for, and the problems of, obtaining effective random cross-fertilization and securing equal maternal contributions is related to random drift and the need to know

the appropriate breeding system, pollination method and pollinators. Optimal cultural conditions are essential for the development of high quality seed which is a prerequisite of viability and longevity during storage [52]. In heterogeneous populations the problems of harvesting all plants with uniform ripeness can only be effectively met by harvesting individual plants separately. If the population has to be bulk harvested (as is the case for most genebanks), then a compromise has to be effected, with the emphasis on securing as wide a range of ripe seed as possible [53]. When mature seed is retained by the plant the problem is not great. However, many of the recently domesticated species, particularly forages, and wild and weedy relatives of crop species notoriously shatter seed and this poses special problems in avoiding selective shift.

Variation in flowering time influences phenotypic assortative mating which disrupts the population into extreme types; however, the process is slow unless the heritability is very high [54, 55]. A possible solution is to grow sufficient plants to permit the selection of a large enough number that flower simultaneously [56]. Variation in seed production is more serious and less easily resolved as it involves not only plant production, but also pollinator behaviour. If the desire is to equalize the maternal contribution, the total seed yield of the accession is limited by that of the lowest yielder. Since the importance of the effect on shift and drift increases with the frequency of regeneration, a possible compromise is to save equal maternal quantities for storage and regeneration and bulk the remainder as a multiplication sample for distribution, evaluation and use [57].

Avoiding pollen contamination through effective isolation

Ensuring adequate isolation from pollen exchange among accessions is the single most important step in maintaining genetic integrity and reducing risk during regeneration. Under natural conditions gene flow by pollen can be almost completely counterbalanced by selection against migrant alleles; thus, differentiation may occur in the presence of up to 50% pollen flow, but the selection pressures have to be of a high order – up to 70% to keep the population differentiated in the presence of a pollen flow of 50%~60% [58]. The relationship between the opposing forces of migration and selection are complex, depending on the dominance relationships of individual loci and the inheritance of the characters involved [59,60,61]. In the absence of selection against migrant alleles, such as would be obtained in accession multiplication, even moderate rates of pollen contamination could cause significant alteration [58,62].

There are several ways to achieve adequate isolation, but these depend on the method of pollination (insect or wind) and the reproductive biology of the crop species. In general, isolation is obtained by: 1) spatial or temporal separation; 2) natural or artificial barriers; and 3) hand crossing accompanied by bagging of the inflorescences.

Spatial isolation studies for a number of wind and insect-pollinated species [63,64,65, 65a] all shown significant (>5%) pollen dispersal by both wind and insects can occur over large distances, although this can vary by season, location and species, direction of wind and insect species and their preferences [39]. For example, most wind-dispersed pollen travels much further than animal-dispersed pollen [39]. For seed multiplication of allogamous cultivars, isolation distances in excess of 200m may be a statutory requirement [66,67]. When dealing with a large number of accessions requiring regeneration, isolation by distance is usually not practical. The outstanding feature of both wind and animal pollen travel is its leptokurtic distribution [68,69]. This distribution is influenced by the foraging strategy of the insect pollinators as related to within-plant and between-plant travel [70]. Few studies have investigated gene flow, as opposed to pollen flow, in wind-pollinated plants. In rye grass, *Lolium perenne* over 99% of the genes traveled less than 20m [68] and in beet, *Beta vulgaris*, all genes traveled less than 10m [71]. These values are of an order of magnitude less than the pollen travel observed in these species, and contrast sharply with insect pollinated plants in which gene travel usually exceeds pollen or pollinator travel [39].

Temporal isolation is sometimes practiced on perennial forage grasses [72]. Through cutting, the plots of different accessions are maintained at different stages of development, hence assuring that where crossing is minimal only distant accessions are at the same phenological stage, such as flowering or heading.

Pollen flow can be further interrupted and reduced by intervening barriers of other species, and this has led to the practice of growing isolation plots in standing crops of tall growing species, ie. sunflower, hemp. Several genebanks have exploited this method by establishing seed islands dispersed in crops of winter rye or winter wheat [73] or *Brassica* spp. [74]. Isolation is achieved by 50m separation between the islands and several seed islands may be contained in one field. Each island contains populations of different wind and insect pollinated species, the latter relying on natural pollinators. The assumption is that the pollinating insects remain within a plot, and before approaching another plot they will be attracted by the flowers representing the island plants. Although this method does not ensure the avoidance of any gene flow between accessions, it is relatively simple and cheap and

thus a large number of accessions can be regenerated.

Other methods commonly use artificial (linen, paper bags and other materials) isolations for the period of flowering for wind pollinated species for controlling interaccession pollination [75,76,43]. The bags cover prior to anthesis a single head, 3~4 heads, in a method referred to as cluster bagging, or a whole plot with the intent to encourage cross-pollination and maintain genetic integrity among accessions [77,78]. Supplemental hand-pollination is sometimes required.

The use of screened cages with specially designed hives for honey, leafcutter or bumble bees or flies (hover, blow) for several insect-pollinated crop species is now common [79,43,80,81,82,83]. To save on resources, one accession each of different crop species may be planted under one net or nylon cage. Insect pollinators are released inside the cage at flowering time to enhance pollination within each accession and thus increase yield. However, problems may occur when more than one accession is grown under a cage, and in come cases supplementary hand-pollination may be necessary, eg. wild species of tomato and eggplant. Also insect pollinators may show preference for one species. The USDA tested the ability of cages to restrict gene (pollen) flow [84]; compared seed produced by various races of honey bees [85]; and documented improvements in regeneration quality and quantity - for sunflower and carrot. Purpose-built pollen proof glass or polyethylene houses are effective, but expensive to operate and maintain [88]. An example can be found at the Institute of Grassland and Environmental Research, Wales which uses a rigorous regeneration scheme for all accessions (forage grasses and clovers) using elaborate crossing houses [89].

The use of isolation cages poses several problems. Aside from being expensive and laborious to construct, the shading that results affects plant growth and may distort characterization data, and pollinator foraging behaviour [90.43]. The environment inside a cage may be favourable for pest insects (aphids, mites); severe infestations may be frequent and often difficult to control even with repeated use of pesticides. Their use may result in negative pesticide-pollinator interactions and the need to reintroduce adequate numbers of pollinators. On the positive side, cages may result in the exclusion of pest, such as protecting Cucumis from beetle-transmitted bacterial wilt [91] or other insects that damage plants and/or fruits, which cause reduced seed yield as well as reduced seed vigour.

The ultimate effective isolation is controlled pollination by hand. During the early stages of seed regeneration hand-pollination can produce sufficient seeds, but with

expanded programs for breeding, testing and the handling of large collections with numerous accessions of each species and the need for effective population size to maintain integrity this becomes too laborious and time consuming. Furthermore, natural pollinators are more efficient and effective in producing quality germplasm than by hand.

Pollinator choice and management

By definition cross-pollination simply means the transfer of pollen of one flower onto the stigma of another by a vector. Efforts have focused on the use of commonly available pollinators for specific crop species with significant success using the honey bee, *Apis mellifera*, and the alfalfa leafcutter bee, *Megachile rotundata*, and lesser success with other bee species such as the mason bees, *Osmia* spp. and bumble bees, *Bombus* spp. and some fly species such as syrphids, *Eristalis tenax* and blowflies, *Phormia terranovae*.

The challenges facing genebank curators in using insect pollinators to regenerate cross-pollinated species are numerous and need addressing through research. They include:

1. identify the optimum (most efficient and effective, but not necessarily the most abundant) pollinator for each crop species; this is compounded as many accessions are being regenerated in regions far from their origin with the optimum pollinator lacking at the new site; particularly troublesome are plant species, frequently native ones, which are oligophilic;
2. identify the 2nd and 3rd pollinator species and their relative value;
3. distinguish between visitors to flowers and actual pollinators, i.e. those that collect, transport and deposit compatible pollen;
4. develop a standard methodology for determining optimum pollinators;
5. number of pollinators needed to pollinate flowers in small plots, cages or greenhouses; integration of bee behaviour, plant yield and agronomy into a pollination model to predict the probability of an individual flower being pollinated under various pollinator and flower densities; the number will be different from large-scale field production; need to account for small plot size, pollinator drift, and nearby plant competition;
6. management techniques (equipment and costs) for the different pollinator species varies and needs to be learned or developed; recent introductions of non-Apis pollinators to new regions have met with varying success [92] ;

7. many genebanks have well trained staff in plant sciences to manage plant regeneration, but not in entomology to manage pollinators; also specialized facilities and training may be needed; and
8. introducing oligolectic pollinators to new regions may increase the risk (new diseases, pests) to already existing pollinator species and disturb existing native plant communities.

Characterization & evaluation

Characterization and evaluation are the functions where value is added to each accession. To avoid confusion when building capacity and in general use characterization means analyzing characters which are highly heritable, that can be seen easily by the eye (except molecular characters) and are expressed in all environments (color and morphology). Evaluation referred to analyzing characters not as easily observed visually, such as pathogen or pest resistance or quality characters (oil or protein content, fiber content, fatty acid profile).

Curators must be aware of germplasm users' (especially breeders) needs for information required to register new cultivars and focus on acquiring this information. Agronomic and horticultural data are high priorities, but quality traits and disease-resistance data are also highly desired. Curators must also be aware of new diseases and respond quickly with evaluations for host-plant resistance. Some countries may not be devoting enough time/resources on evaluating germplasm for disease resistance or product quality, sometimes because a standard set of differential lines (isolates) for certain pathogens are lacking. The development of core (or sub-core) subsets is needed for more crop species. Core subsets provide one rational mechanism for managing the genetic diversity within a collection.

Considering its global importance, it is striking that climate change is rarely mentioned in rationale or objectives for most gene banks. Curators and managers should assume a proactive role in preparing for this so as to minimize future crop production risk. Relevant germplasm should be acquired, new descriptor criteria (eg. resistance to drought, salinity, identification of stress tolerant genes) and techniques developed, and germplasm evaluated for those factors.

Examples of characterization & evaluation research to reduce risk

Analyses of phenotypic variation for 10,050 accessions of hexaploid cultivated oat were completed. Eight environmentally stable morphological characters differentiated the germplasm into 18 character states. Comparisons of oat diversity from different countries, among the major infraspecific groups and among Canadian oat cultivars registered between 1886 and 2002 were possible. The number of accessions in each morphological group was unevenly distributed with the 13 most frequent morphological groups representing 90% of the accessions. The most frequent morphological groups were identical to the most frequent types of Canadian oat cultivars. The greatest richness of diversity was found in oat from countries with temperate climates and intensive oat breeding programmes. The oat accessions comprised 8754 accessions of common hulled oat, 183 accessions of hull-less oat and 1168 accessions of red oat. For red oat *(A. sativa* (=*A. byzantina* C. Koch)), West Asia was richest in diversity. The USA could be considered a secondary centre of diversity for red oat and Canada a secondary centre of diversity for hull-less oat [93].

Modern molecular tools, such as AFLP (amplified fragment length polymorphism), SSR (simple sequence repeat) and DNA sequencing, are being used to characterize genetic diversity in plant and animal populations. Effective genetic analyses including Bayesian and stochastic modeling approaches are applied to partition genetic diversity within and among populations, whereas phylogenetic reconstruction methods retrace and illustrate molecular ancestry and relationships among the plant or animal groups of interest. Various diversity functions (Weitzman and Marker Estimated Kinship) help set priorities in plant and animal germplasm.

Germplasm characterization with molecular genetic markers has increased substantially. Although genetic marker information provides new insights into intrinsic genetic variability, the analyses and application of genetic markers involve many challenges. National workshops to discuss these challenges and of integrating molecular data into practical gene bank research would be valuable. They could address the optimal types of marker, strengths/weaknesses for specific purposes, and the appropriate number of markers. For some crops, it may be more efficient to involve industry or university partners or to farm-out genetic marker analyses rather than to develop the expertise “in-house.” This approach may increase interaction, take advantage of their expertise, increase utilization of collections and enhance capacity building within and among nations.

Diversity analyses based on molecular and agrobotanic studies have been conducted on wild and cultivated germplasm of flax [94,95,96] and oat [97,98,99] and several oilseed crucifer species [100]. These studies have resulted in more efficient germplasm conservation, and useful germplasm has been identified and integrated into breeding programs. Molecular analyses of the genetic diversity of wheat [101,102], soybean [103] and several native Canadian grass species [104,105,106,107,108,109] have also justified the need for germplasm conservation.

AFLP analysis of 163 accessions of 25 *Avena* species with diverse geographic origins was completed. This analysis revealed 59.5% of the total AFLP variation resided among 25 oat species, 45.9% among six assessed sections of the genus, 36.1% among three existing ploidy levels, and 50.8% among eight defined genome types. All the species were clustered together according to their ploidy levels. The C genome diploids appeared to be the most distinct, followed by the Ac genome diploid *A. canariensis*. Analysis of AFLP similarity suggested that the AC genome tetraploid *A. maroccana* was likely derived from the Cp genome diploid *A. eriantha* and the As genome diploid *A. wiestii*, and might be the progenitor of the ACD genome hexaploids. These AFLP patterns are significant for our understanding of the evolutionary pathways of *Avena* species and genomes, for establishing reference sets of exotic oat germplasm, and for exploring new exotic sources of genes for oat improvement [110].

SSR analysis of 169 potato accessions representing diverse geographic origins was completed. This analysis showed 2.4% of the total SSR variation resided among accessions of different countries, 0.8% between Canadian and exotic potato accessions, 3% among Canadian accessions of four breeding periods defined, and 0.8% between Canadian heritage and non-heritage cultivars. These findings demonstrate the narrow genetic basis of potato germplasm and justify the need for broadening the improved potato gene pool. In spite of this, the most genetically distinct potato germplasm was identified for potato improvement [111].

The Microbial collection has contributed to research on several plant diseases and mycotoxins and provided information to national and international clients. Initial efforts to develop broad-spectrum diagnostic kits to detect *Carlaviruses* have been successful and prototype RT-PCR primer sets were used to detect and sequence two new highly divergent strains of Blueberry scorch virus in BC.

Evaluation of disease resistance in chickpea, canola and lentil relies on fungal isolates representing pathotypes, inoculation in growth chambers and verification with natural

infection in a cold-frame greenhouse. The genetics of resistance inheritance will requires the segregation of resistance in F_1, F_2 and backcross generations, populations of doubled haploid lines and/or recombinant inbred lines. Mapping of sclerotinia resistance involves microsatellite markers, and mapping of ascochyta resistance will use single nucleotide polymorphism.

Indoor disease screening methods were developed for lentil, canola, bean, sunflower, soybean and chickpea and a 4000 sq ft cold-frame greenhouse was built for screening under natural infection; QTL's conferring sclerotinia resistance in canola were identified, and data on 1500 lentil accessions of which 35 were resistant to anthracnose were placed in GRIN-CA. Bioactive substances in diverse germplasm of pea and lentil have been isolated and identified.

Evaluation of canola (*B. napus*) germplasm for resistance to the fungal pathogen *Sclerotinia sclerotiorum* the cause of stem rot: QTLs conferring resistance to sclerotinia stem rot in the Chinese cultivar Zhong You 821 (ZY821) were mapped in 6 DH and 3 RIL populations. So far, QTLs have been identified on LG 1, 3 and 19. *B. napus* germplasm from PGRC, Dr. Rakow (AAFC, SRC), and the Nordic and Czech gene banks were screened for stem rot resistance; up to now, 10 new lines, obtained from Kashmir and Pakistan, have high levels of stem rot resistance. New methods for production of ascospores under controlled conditions and inoculation of canola stems, with ascospores on petals as nutrient source, were developed. Two sclerotinia nurseries were used to screen selected resistant and susceptible DH lines and germplasm under field conditions; however, inoculation of the soil with sclerotinia (survival structures) created variable inoculum pressure confounding the disease rating; consequently, inoculation of individual plants with ascospores on petals is now used. A micro array study of genes differentially up or down regulated in infected versus un-infected stem tissue, and susceptible versus resistant tissue were conducted and approximately 50 potential defence genes were identified.

Bioactive compound identification and seed oil evaluation uses various chromatographic techniques (medium pressure liquid, flash, thin-layer and gas) as well as electrospray – ionization, and matrix-assisted laser desorption/ionization mass spectrometry, and high-resolution NMR spectroscopy; concentrations will be assessed using HPLC with evaporative light scattering and photodiode array detectors.

Six chickpea seed samples supplied by Crop Development Centre, University of Saskatchewan were ground and flour samples (1-gram scale) extracted at ambient

temperature with 80% methanol. The crude extracts, treated briefly for 7 days with ordinary fluorescent light, were cleaned with Diaion HP-20 beads before soyasaponin analysis by HPLC. Defatted flours (100g) of the yellow field pea, green field pea, lentil, dry bean and soybean were processed in methanol with brief and 3 days of fluorescent light exposure in a chamber. The HP-20 methanol fractions from these extracts were isolated and examined by HPLC and electrospray LC/MS. The best source of dehydrosoyasaponin I was Amit chickpea followed by soybean and yellow field pea. Data was tabulated and submitted for inclusion into a PCT application.

Raw Amit chickpea flour (100 g scale), a controlled environment chamber maintained at 21C and equipped with 6x40 Watt fluorescent lights of the Cool White type (intensity of about 2250 lux at the centre of the chamber) proved to be an excellent visible light source for the generation of dehydrosoyasaponin I from soyasaponin VI. The utility of this chamber was demonstrated in two experiments with 80% methanol (48 hour light exposure) and two experiments with 60% ethanol (72 hour light exposure) as extraction solvent. Resulting Diaion HP-20 methanol (and ethanol) fractions enriched in dehydrosoyasaponin I (and soyasaponin I) were studied in detail by TLC, HPLC and electrospray LC/MS. Using these fractions (50 mg/injection), it was demonstrated that dehydrosoyasaponin I could be isolated in milligram quantities by medium pressure liquid chromatography with a custom-prepared reverse phase column of styrene/divinyl benzene (Source™ 15 RPC) and a gradient of ammonium hydroxide plus acetonitrile. Data was tabulated and submitted for inclusion into the PCT application.

Research on animals uses standard procedures for collection of germplasm from livestock and poultry breeds, extraction of proteins, Western blotting, immunolocalization, SDS-PAGE, 2-D electrophoresis, RT-PCR, and *in situ* hybridization. *In vitro* production of swine embryos depends on three techniques: *in vitro* maturation of oocytes, *in vitro* fertilization, and *in vitro* culture of embryos. Modifications to conditions and media are implemented to optimize embryo production. To transfer pig embryos, non-surgical methods are being developed. Modification of cryo-media and cryopreservation protocols are being developed to preserve bull, boar and rooster semen. Vitrification techniques are being used to preserve oocytes and embryos from different species.

Documentation

A computerized database management system (GRIN-CA) to handles the massive amount of data collected by PGRC, the Clonal Gene bank, the Nodes and the Animal Genetic Resources Program. The database software was acquired from the USDA, Database Management Unit, Beltsville, MD which means that all plant genetic resources in North America use the same database system. A new database structure is being developed for the animal program in cooperation with the Animal Genetic Resources Unit, Ft Collins, CO and EMBRAPA, Brazil. Combined, these systems with common programming language increase the programming capability and reduce the risk to loss data. The computer hardware/operating system used in Canada is a Sun/Solaris with an Oracle user interfaces supplemented by MVC web technology and traditional HTML. Timely back up of program language software and all data is essential to reduce risk of loss. Periodic placement of data at another location is highly desired.

Increased emphasis is being placed on digital imaging, especially when images of different organs (seed, flower, roots) are being captured so as to provide validity to descriptor characters. The next step will be to apply new technologies to numerically scan the images and generate numerical data as well. A major effort is still required to incorporate genetic marker data into GRIN-CA and this will be challenging.

Capacity building

Capacity building in Canada takes many forms. A senior undergraduate course in plant genetic conservation and utilization is offered by genetic resource staff in the Plant Science Department, University of Saskatchewan. Animal genetic resource staffs offer several lectures in animal genetic resource conservation within the Animal/Poultry Science Department and the Western Veterinary College, University of Saskatchewan. The ultimate aim here is to develop a formal graduate degree granting program in animal genetic resource conservation. Training of a number of undergraduate, graduate and post doctoral students occurs as do numerous shorter term visits by international colleagues. Numerous tours of facilities and collections are given to scientific and producer societies or organizations, parliamentarians, visiting delegations and school groups. Written productivity takes the form of peer reviewed scientific publications, posters, technical reports, abstracts, book reviews, book chapters and numerous presentations at scientific and producer meetings.

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Risk Management of Microbial Genetic Resources in the BCRC/FIRDI of Taiwan

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Abstract

Microorganisms, their cells and replicable parts (e.g. genomes, plasmids, viruses, and complementary DNAs) are the tools for biotechnology and underpin the life sciences. They provide a major source of genetic information to solve problems in agriculture, industry, plant and animal sciences, and human health. The total number of microorganisms is unknown, and they are difficult to study *in situ*. Microorganisms that are isolated from natural and manmade environments are typically conserved in microbial resource centers (MRCs). It has been over two decades since 1982, when the Bioresource Collection and Research Center of the Food Industry Research and Development Institute (BCRC/FIRDI) initiated the work of microbial resource collection and preservation in Taiwan. In 2001, the quality management system of BCRC/FIRDI was audited and determined to be compliant with ISO 9001:2000 requirements. Being a multifunctional MRC, the BCRC/FIRDI implements access and benefit sharing (ABS) by establishing a biological material transfer mechanism and being involved in benefit-added biological material development. The BCRC holds three domains of bioresources: microbial resources, cellular resources, and genetic resources. In order to ensure the availability, integrity, and traceability of all records concerning these bioresources, we developed a workflow management system. The first step in risk management processes is to identify vulnerabilities and threats and then to assess the possible damage to determine where proper countermeasures should be implemented. All challenges require efforts not only from individual MRCs, but also from cooperation among MRCs, particularly internationally. In the future, the BCRC will continue to provide high-quality cultures, and genetic information facilities and techniques. The BCRC aims to support and promote partners engaged in general and applied research to enable them to accelerate their research and contribute to the development of the bio-industry in Taiwan.

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Introduction

Microorganisms, their cells, and replicable parts (e.g., genomes, plasmids, viruses, and complementary DNAs) are the tools for biotechnology and underpin the life sciences. They provide a major source of genetic information to solve problems in agriculture, industry, plant and animal sciences, and human health. The diversity of microorganisms plays a major role in maintaining the biosphere and provides vast resources for mankind. The total number of microorganisms is unknown, and they are difficult to study *in situ*. They may be transferred across borders by wind, water, and the movements of animals and humans. They are unlikely to be depleted by sampling; however, the loss of hosts can lead to the loss of dependent microbial species. Microorganisms that are isolated from natural or manmade environments are typically conserved in microbial resource centers (MRCs), be they public-service MRCs or specialized research MRCs. For the purposes of describing new taxa and acting as essential reference standards for future study and use, the conservation and accessibility of type strains (those on which the taxonomic description is based) and other representative isolates are fundamental. Furthermore, the *ex situ* conservation of all isolated microorganisms that have been studied and reported in the scientific literature would equally be important if science is to progress. The uncertainties associated with the re-isolation of strains underline the need for deposition in an MRC, where conservation skills and ready accessibility to specimens tagged with a conserved and unique reference number are provided. Without this, scientists would constantly need to conduct the skilled and expensive processes of isolation, characterization, and identification at the beginning of each new study. Careful documentation of all conserved materials and the availability of such data are essential tasks of MRCs.

Roles of MRCs

MRCs are the custodians of microbial diversity and play a key role in the storage and supply of authentic reference materials for research and development. MRCs are often regarded as living libraries and represent dynamic institutions of learning, research, scientific culture, and information. MRCs must be established with utility, particularly to serving scientific, industrial, agricultural, environmental, and medical research, and development of biotechnological applications, while providing protection for intellectual property. The benefits of the conservation and sustainable use of microbial resources, emphasized by the *Convention on Biological Diversity* (CBD), highlight the role of MRCs as *ex situ* protectors of

biodiversity. They also offer an important interface among governments, industry, and the public, helping policy makers and the public understand the value of conserving microbial resources.

Development of an MRC in Taiwan

The development of a microbial resource collection of Taiwan began in 1978. The idea of establishing an MRC was initially discussed at the first National Science Conference formally held in the same year. At the meeting, one important item was on the agenda: to preserve microbial cultures for industry.

In 1982 when the second National Science Conference was held, four science projects included ”Biotechnology” and ”Food technology” were added as the 7th and 8th national policy research projects. The Culture Collection and Research Center (CCRC) was then established in the Food Industry Research and Development Institute (FIRDI), a non-for-profit independent research institute, to support the project of the Ministry of Economic Affairs (MOEA) for industrial purposes in 1982.

It has been over two decades since 1982, when the CCRC/FIRDI initiated the work of microbial resources collection and preservation. The CCRC/FIRDI then became a member of the World Federation for Culture Collections (WFCC) in 1984. In 1987, on the initiative of the Council of Agriculture (COA) of the Executive Yuan, a long-term "Agricultural Microorganisms Bank" project was also assigned to the CCRC. An amendment to the Patent Law in 1994 allowed public ownership of microbial patents. The MOEA designated the CCRC/FIRDI as the national depository for microbial-related patent applications with the support of the government Intellectual Property Office (IPO). In 1998, the CCRC became a core facility of the National Health Research Institute (NHRI) as a cell bank to support the development of biomedical research. In 2001, the CCRC initiated a microbial genome project. The CCRC was then renamed in 2002 as the Bioresource Collection and Research Center (BCRC).

Challenges and opportunities for MRCs

It is time for changes in traditional culture collections. Operations of microbial collections have changed over the last decade as a result of advancements in bioinformatics and in the ability to present electronic data over the internet. In addition, the huge gap between the discovery of new microorganisms and their potential numbers in nature has stimulated an interest in microbial diversity and harnessing their genes, properties, and

products. Therefore, implementation of international criteria for quality management is now essential for MRCs to provide reliable and high-quality microbial resources and authentic information. MRCs now need to provide access to genes and genetic elements with associated information. Long-term and stable preservation of microbial resources is a crucial obligation of MRCs.

The CCRC was renamed in 2002 as the BCRC in accord with the expansion of collections of cells and genetic resources. Simultaneously with the name change from CCRC to BCRC, the center was reorganized into five working fields: (1) microbial resources, (2) cellular resources, (3) genetic resources, (4) development of bioresources, and (5) services for bioresources. The center was also subdivided into 13 working groups (Table 1). The functions and service platform of BCRC in Taiwan is shown in Figure 1.

Table 1. Structural framework of the BCRC/FIRDI

Working field	Working group
Microbial resources	Bacteria and yeasts
	Filamentous fungi
	Mushrooms
Cellular resources	Human and animal cell lines
	Stem cells
Genetic resources	Gene bank
	Functional genomics
	Bioinformatics
Development of bioresources	Genetic resource development
	Microbial resource development
	Fermentation
	Bioengineering processes
Services for bioresources	Bioresource services

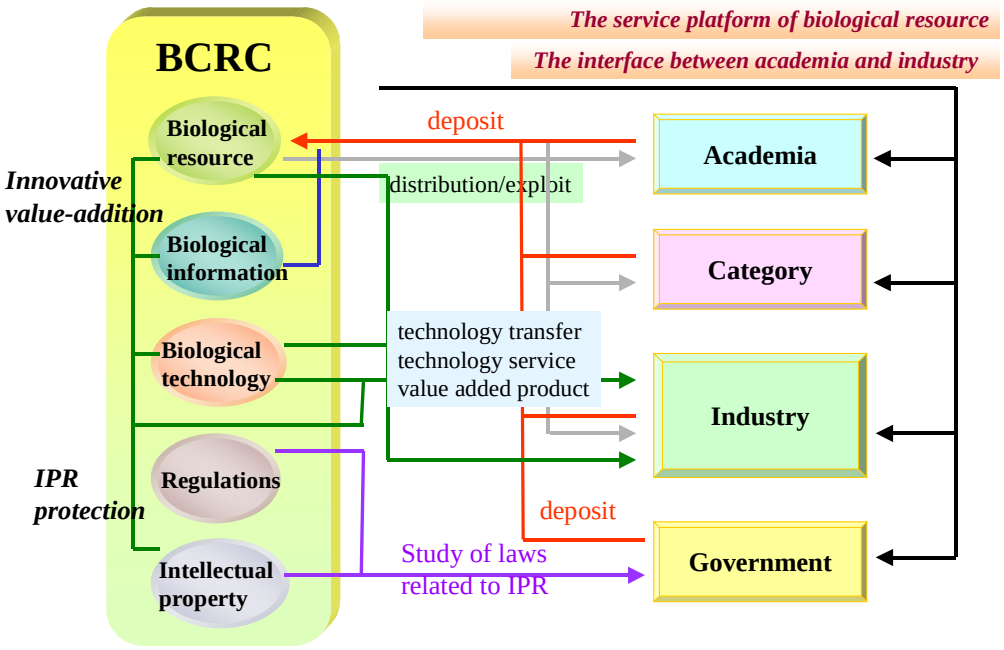

Figure 1. The functions and service platform of the BCRC/FIRDI in Taiwan

Establishment of an ISO quality management system at the BCRC/FIRDI

In 2001, the quality management system of the BCRC/FIRDI was audited and found to be compliant with ISO 9001:2000 requirements. The quality management system includes (1) a patent-related biological material depository, (2) contract microbial identification and tests, (3) cultivation and preservation of animal and human cells, (4) collection, preservation, and distribution of microbial resources, and (5) collection, preservation, and distribution of genomic and complementary DNA libraries.

The quality policies of BCRC in ISO 9001 include biodiversity, systematic management, professional services, and quality at the international level (Table 2).

Table 2. Quality policy statement of the BCRC/FIRDI

Biodiversity
1. Conserving biodiversity in the sprit of the *Convention on Biological Diversity* (CBD).
2. Offering services based on the diverse collection of bioresources.
Systematic management
1. Establishing documentation systems and standard operation procedures for all service processes.
2. Establishing an efficient, low-cost, and satisfaction-guaranteed management system.
Professional services
1. Establishing techniques for professional services.
2. Establishing service credibility.
Quality at the international level
1. Establishing a quality management system that meets ISO 9001 standards to achieve an international level of quality.
2. Ensuring satisfaction with products and services to establish a bioresource collection and research center of international standards.

Risk management of bioresource information and MRCs

The BCRC holds three domains of bioresources: microbial resources, cellular resources, and genetic resources. In order to ensure the availability, integrity, and traceability of all records concerning these bioresources, we developed a workflow management system to collect and manage all documents, information, and tasks from one participant to another for actions according to the procedural rules of deposition, preservation, storage, and distribution that are ISO 9001:2000 certified. To date, 891,701 bioresources are being held in the BCRC, and 971,645 related data are stored in the in-house database. External and internal users access the data through the internet and intranet. More than 650,000 man-hours are used to browse bioresource-related information per year. Therefore, information security is an important on-going issue for the BCRC. Risk management processes in terms of security should be considered.

The first step in risk management processes is to identify vulnerabilities and threats and then to assess the possible damage to determine where proper countermeasures should be implemented. The assets associated with information should be quantitatively and qualitatively measured, which will be helpful in determining the proper plan to reduce the

aspects affected by different threats. In the computerized environment of the BCRC, it is easy for web users such as hackers, employees, and contractors to exploit system vulnerabilities to cause harm to the network, databases, or online services. The tangible value of information assets is estimated to be at least TWD 4 billion. If there was irreversible impairment of the assets, they could be reconstructed. But the impact due to the loss of data, information, and intellectual property on BCRC's business and reputation would be inestimable. The best practice for BCRC's business continuity is to address each risk individually.

Countermeasures implemented by the BCRC are to reduce overall risks to an acceptable level. With strategies of building up prevention controls by monitoring safeguards such as firewalls, antivirus software, and vulnerability scanners, the risk from hackers and viruses can be reduced. To prevent unwanted incidents, all possible disasters are predicted, and annual disaster drills are planned and executed in case those events do actually occur. Once a disaster occurs, in order to rescue computer servers from irreversible damage, a recovery solution to reset and return the servers to their original configurations from a backup site is required. The damage can also be ameliorated by executing viable alternatives such as switching to mirrors which are synchronized with the production and which serve as a redundant environment to maintain the system performance during an emergency.

Access control by employees and contractors is hard to deal with using IT tools. Access authorities are defined according to the skill identification and management responsibilities. The system will look at some types of access control matrixes or compare security labels to verify that a subject may indeed access the requested resource and perform the attempted actions. But training and awareness programs should continually be implemented to prevent security incidents by staff members. The BCRC also executes regular monitoring and review procedures by auditors to determine and measure the effectiveness of its risk management. The last approach is to accept the risk, face the potential costs of damage, and then institute appropriate corrective controls to eliminate the cause of nonconformities in order to prevent a recurrence.

The major risks and strategic plans for risk management of an MRC by the BCRC/FIRDI in Taiwan are summarized in Table 3.

Table 3. Risk management of a microbial resource center by the BCRC/FIRDI

Type of risk	Risk	Strategy for risk management	
Collection of microbial genetic resources (MGRs)	Loss of local MGRs with unique properties	Exploit	Set up a special collection system to facilitate the collection of local MGRs
	Loss of scientific research achievements	Share	Publish "regulations for grants, deposits, and distribution of biological material"
	Limitations on the distribution of international bioresources	Enhance	Set up a service platform for bioresource distribution; Assist the importation of international bioresources
	Limitations on the acquisition and benefit-sharing of bioresources	Exploit	Actively participate in international cooperation (e.g., MOSAICS) to establish standards
	Limitations on isolation and preservation abilities	Enhance Share	Develop new isolation and preservation technologies; Promote cooperation with local research communities
Preservation of MGRs	Limitations on the preservation ability	Mitigate Enhance Exploit	Employ multiple types of preservation to reduce risks; Establish new preservation technologies; Establish a banking system for genetic resources
	Limitations on the identification and authentication abilities	Enhance	Develop new identification technologies

	Quality control	Enhance	The BCRC has received ISO Standard 9001 accreditation since 2001 and has maintained its quality assurance system with no nonconformities; Incorporate BRC guidelines
	Management of facilities	Mitigate Transfer Enhance	Establish backup systems to reduce risks; Acquire maintenance contracts for risk transfer; Maintain the best practices by continually renewing facilities
	Resource management	Transfer Enhance	Purchase insurance for the storage environment; Incorporate the ISO 9001:2000 quality assurance system
	Information technology ability	Enhance	Develop a workflow management system to collect and manage all documents and information; Build up prevention controls by monitoring safeguards
Distribution of MGRs	Distribution control for potentially hazardous microorganisms	Enhance	Develop a material transfer mechanism for appropriate management of access to and transfer of microbial resources
	Convention on Biological Diversity Quarantine regulations	Exploit Enhance	Actively participate in establishing standards (e.g., patent depository, regulations on genetic resources); Set up a service platform for bioresource distribution
	Packaging and transport control	Enhance	Comply with international regulations
	Customer relationship Management	Share	Create the greatest benefits for MRCs by customized and value-added technological services

Establishment of a biological material transfer mechanism at the BCRC/FIRDI

Being a multifunctional MRC, the BCRC/FIRDI implements ABS by establishing a biological material transfer mechanism and being involved in benefit-added biological material development.

For the transfer mechanism, the BCRC/FIRDI enacted a “regulation for deposits, donations, and distribution of biological materials” in 2003. The regulation, including material transfer agreements, sets out basic contract terms among biological material providers, recipients, and the BCRC/FIRDI. First, providers are encouraged to obtain prior informed consent from the country of origin. Second, providers may further define the terms they require, such as benefit-sharing provisions. The terms required by providers bind the recipients. The mutually agreed-upon benefit-sharing terms between providers and recipients are made possible by the bridge of the BCRC. Third, further transfer of materials from recipients to any third party is prohibited. Limiting further transfer to third parties can shorten the transfer chain along which microbial resources may be lost to monitoring of the transfer.

Along the microbial resource transfer chain, from an *in situ* resource origin to an *ex situ* resource isolator to an MRC to an *ex situ* resource user, being an important collector and provider for *ex-situ* microbial resources enables an MRC to monitor and track the resource flow (Figure 2). Thus, an MRC can play a role in realizing the ABS concept. First, an MRC can encourage prior informed consent by requiring proof of that consent when acquiring microbial resources from a provider. Second, by using a material transfer agreement in a biological resource center (BRC), the bridge of the MRC can facilitate the creation of mutually agreed-upon terms between providers and users of microbial resources.

Using molecular characterization of 852 of groundnut accessions using 21 SSR markers, we secured allele information on rare and unique alleles for hypogaea, and fastigiata cultivar groups and wild species accessions and accessions of geographic origin – Africa, America, Asia, Europe, and Oceania. The gene diversity in groundnut composite collection was 0.819. Wild relatives were more diverse than sub-species hypogaea and fastigiata. Groundnut accessions from Americas were more diverse followed by Asia and the gene diversity was minimum in germplasm accessions from Oceania.

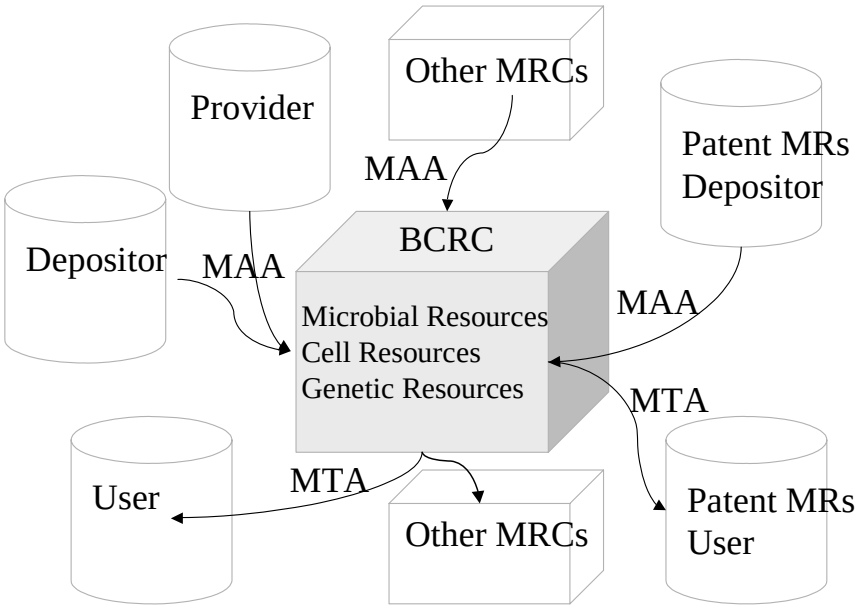

Figure 2. Transfer of microbial resources (MRs) from providers to users through the BCRC material transfer mechanism

The FIRDI was designated the national authority for the deposition of patent-related biological materials with the support of the government IPO in 1994. The patent-related depository work is processed based on “The Regulations and Rules of Microorganisms Deposits for Patent Purposes” and the standard operation procedure (SOP) of the quality control system (ISO 9001:2000). After acceptance of each case, the institute tests the deposited microorganisms for viability and then preserves them. To ensure the safety and confidentiality of the deposition, microorganisms and related documents and the storage room are operated under strict managerial regulations. Patented microorganisms are available to the public for research purposes upon request until the patent is granted. At the end of September 2008, the BCRC/FIRDI had accepted over 1500 microorganisms deposited for patent purposes of various types and from various countries.

As to issues of the transfer of microbial resources, there are national regulations about importation controls of microbial materials in Taiwan (Table 4).

Table 4. Importation controls of microorganisms and related materials in Taiwan

Governing issues	Plant protection	Animal protection	Human protection	Environmental protection
Governing authorities	Plant Division, The Bureau of Animal and Plant Health Inspection and Quarantine (BAPHIQ), Council of Agriculture, Executive Yuan	Animal Division, The Bureau of Animal and Plant Health Inspection and Quarantine (BAPHIQ), Council of Agriculture, Executive Yuan	Centers for Disease Control (CDC), Department of Health, Executive Yuan Bureau of Medical Affairs, Department of Health, Executive Yuan	Environmental Protection Administration, Executive Yuan
Related laws and regulations	*Plant Protection and Quarantine Act*	Statue for Prevention and Control of Infectious Animal Disease	*Communicable Disease Control Act* Regulations Governing Management of Infectious Biological Materials and Collection of Specimens from Patients of Communicable Diseases Statute For Transplantation Of Human Organs	*Environmental Agents Control Act* Regulation Governing Experimental Research for the Purpose of Developing Environmental Agent Using Genetic Engineering Microbial Preparations

Perspectives

Intellectual property rights (IPRs) are one of the efforts required from MRCs. Numerous challenges still remain in facilitating the exchange of microbial resources and technologies. For example, restrictions affecting access to microbial resources must be managed to accelerate the exchange process. Monitoring and tracking of microbial resources are priorities for realizing access and benefit sharing, and consequently can encourage resource exchanges. All challenges require efforts not only from individual MRCs, but also from cooperation among MRCs, particularly internationally. In the future, the BCRC will continue to provide high-quality cultures, and genetic information facilities and techniques. The BCRC aims to support and promote general and applied research partners to enable them to accelerate their research and contribute to the development of the bio-industry in Taiwan.

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Conservation and Utilization of Genetic Resources in Canada

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Abstract

Canada manages a distributed repository system for plant, animal and microbe genetic resources, integrated to increase efficiency through commonality of functions. This public-good service-oriented research provides high quality germplasm and well documented information to national and international clients dealing with crop and livestock production, improvement and bio-based product development. The research is specific to the conservation and utilization of genetic resources. Genetic resources and associated information are believed to play a fundamental role on an ongoing basis to most fields of biological science because, they provide insurance of supplying basic materials for agriculture and agri-food against future adverse conditions; preserve germplasm of useful traits such as resistance to new pests, adaptability to climate change, other environmental conditions or compounds for bio-based products; inputs into inspection and regulatory matters; and provide stability to farming systems at the local, national and international levels by smoothing yield variability through maintenance of a wide range of diversity. All these ultimately impact Canada's ability to trade internationally. Canada's research effort in the conservation and utilization of genetic resources is worthy as generates positive policy, environmental and social impacts. As biodiversity has been identified as an important contributor to society's mental and physical well-being, being able to conserve and describe the genetic diversity and variation of plants, animals and microbes plays a major role in support of this well-being.

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Introduction

Canada through Agriculture and Agri-Food Canada, has managed and conserved genetic resources for more than 37 years. Plant Gene Resources of Canada (PGRC) initially located in Ottawa, Ontario and re-located in 1998 to the Saskatoon Research Centre, Saskatoon, SK was established in 1970 with the mandate to protect, preserve, and enhance the genetic diversity of plant species of economic importance and their wild relatives. The Clonal gene bank at the Greenhouse and Processing Crops Research Centre, Harrow, Ontario followed a few years later as did the Potato Repository at the Potato Research Centre, Fredericton, New Brunswick. Management responsibility for two microbial collections, the Canadian Collection of Fungal Cultures at the Eastern Cereal and Oilseed Research Centre, Ottawa and the Plant Virus collection at the Pacific Agri-Food Research Centre in Summerland, British Columbia were added. The most recent addition to the national program in May 2006 was a domestic Animal Genetic Resources program co-located in the University of Saskatchewan (Western College of Veterinary Medicine and the Animal and Poultry Science Department), Saskatoon. In this distributed repository system stretching across Canada, about 50 professional and technical staff members have expertise in crop breeding, horticulture, entomology, plant pathology, population genetics, reproductive physiology, cryobiology and bioinformatics. All basic functions of gene banks are conducted including acquisition, distribution, maintenance, regeneration, characterization, evaluation and documentation. Efficiencies of operation and management have been obtained through integration of plant, animal, microbe and plant virus collections.

During summer/fall, 2006 the Federal Minister of Agriculture conducted a series of consultations across Canada to determine the science priorities for the government and Agriculture and Agri-Food Canada. Consultations were obtained from a wide audience including farm producers, marketers, academics, provincial extension personnel, public and private agri-industry representatives. Seven priority areas were identified:

1. Enhanced human health and wellness through food and nutrition and innovative products;
2. Enhancing the quality of food and the safety of the food system;
3. Enhancing security and protection of the food supply;
4. Enhancing economic benefits for all stakeholders;
5. Enhancing environmental performance of the agricultural system;
6. Understanding and conserving Canadian bioresources;

Science deliverables:

* availability of information on the classification/attributes of bioresources
* availability of science based tools and knowledge to predict the behavior of biological resources in response to environmental change

7. Developing new opportunities for agriculture from bioresources

From these consultations a peer review research proposal process was developed to encompass all research being conducted by AAFC. The Canadian Genetic Resources Program obtained strong positive comments on its proposal and was full funding for 4 years. Recently the Animal Genetic Resources program has received new and additional funding through a Risk Mitigation initiative. The Program clearly fits under national Priority #6 with the following long-term and short-term objectives.

Long-term objectives are to protect and conserve the genetic diversity of Canadian bioresources, contribute to the security, protection and safety of the food system, enhance the environmental performance of the Canadian agricultural system, contribute to the development of new opportunities for agriculture, thereby enhancing food and feed quality, Canadian health and wellness, and economic benefits for the industry, and support bioresource-related regulatory requirements. Short-term objectives are to: a)develop new techniques to conserve and regenerate plant, animal and microbial germplasm to maintain genetic integrity and minimize genetic erosion; b)create new phenotypic and genotypic information including identifying new sources of disease resistance, abiotic stress resistance, nutritional quality and bioactive compounds, through characterization and evaluation of bioresource attributes; c)assess genetic diversity changes in domesticated plant and animal germplasm; d)improve the structure of the GRIN-CA database for delivery of bioinformation; and e)contribute to access and benefit sharing regimens (acquire, donate, maintain, regenerate germplasm) consistent with Canada's commitments to international treaties, e.g. Convention on Biological Diversity (CBD) and the FAO International Treaty on Genetic Resources for Food and Agriculture (ITGRFA).

The Program objectives have high relevance to AAFC priorities: They are aligned with, and create the basis for, enhancing our understanding of Canadian bioresources, and protecting and conserving their genetic diversity (Priority 6). Deliverables include the development of information and technologies associated with acquisition, conservation, regeneration, characterization, evaluation and documentation of plant, farm animal and

microbial bioresources. This research is essential to the conservation of Canadian bioresources, to ensuring a supply of diverse germplasm to face adverse conditions, to the development of adaptation strategies to climate change, and to support regulatory requirements. The objectives contribute to: a) developing new opportunities for agriculture from bioresources, and enhancing human health and wellness through food, nutrition and innovative products (Priorities 7, 1), through development of information on the composition, structure and possible applications of bioresources that can contribute to the bioeconomy; b) enhancing economic benefits for industry and environmental performance of the Canadian agricultural system (Priorities 4, 5), through identification of useful germplasm which will contribute to cultivar improvement, the reduction of production risk factors, and the reduction of pesticide use, thus improving management practices and reducing soil and water contamination from pathogens and pesticides; and c) enhancing the quality and supply of food and the security, protection and safety of the food system (Priorities 2, 3), through contributions to the development of tools, techniques and strategies for the detection and mitigation of microbial threats to the safety, security and protection of Canadian food production and distribution systems. This meets Canada's legally binding commitments to international treaties and conventions such as the Convention on Biological Diversity (CBD) and the International Treaty on Genetic Resources for Food and Agriculture (ITPGRFA).

Current holdings

Plant Gene Resources of Canada (PGRC) maintains, and conducts research on an *ex situ* collection of about 110,800 accessions of plant germplasm at: a) Saskatoon (1050 plant species: 107,000 accessions); b) Harrow (fruit trees and small fruits: 3,500 accessions); and c) Fredericton (potatoes: 139 clones); the Canadian Collection of Fungal Cultures maintains 14,000 strains, the Canadian Plant Virus Collection maintains 550 isolates of 230 different viruses and the Animal Genetic Resource Program already has over 250,000 doses of semen and 85 embryos from 16 cattle breeds, over 1100 semen doses from elk and bison, over 1400 blastodermal cells from 42 poultry lines and about 500 semen samples from chicken and turkey breeds.

Development of new techniques to conserve and regenerate plant, animal and microbial germplasm to maintain genetic integrity and minimize genetic erosion

Outdoor germination experiment on 16 native Canadian plant species included germination in a replicated experiment using 4 soil types. A study was continued on the application of germination promoters (including GA_3, KNO_3, and ethylene) for the germination of native plant seeds; initiated the development of a protocol using the vital dyes fluorescein diacetate and sytox green for the determination of seed viability.

Continued evaluations of fabric tents for isolation increase of crucifer germplasm. Tents constructed with durable material require less maintenance than commercially available tents and provide some frost protection for later maturing germplasm.

New protocols for production of *Sclerotinia sclerotiorum* ascospore under controlled conditions were developed along with a new protocol for inoculation of *Brassica napus* with ascospores on petals of *Arabidopsis taliana*.

Research was initiated on in vitro produced pig embryos. Agreements were developed to obtain a constant supply of ovaries from a local abattoir.

Collaborations were initiated with scientists at the University of Saskatchewan studying bison reproduction and the development of a new extender to improve sperm cryopreservation in cattle. With the bison group two grant proposals were successfully submitted related to the application of reproductive technologies for bison and on *in vitro* fertilization to evaluate semen frozen with different extenders.

A new mechanism of programmed cell death in bull sperm was developed. Sperm proteins harvested from fresh and frozen semen of different bulls, and egg yolk containing extender were subjected to SDS electrophoresis and 2-D electrophoresis to quantify heat shock protein-70 and caspase-3, proteins involved in somatic cell death. Both proteins are present in fresh and frozen sperm, but their patterns varied. The expression of caspase-3, and executioner protein, increased significantly after freezing and processes. This phenomenon was further investigated and found that egg yolk contributes a significant amount of caspase-3 to sperm cells during freezing process. This study will help to understand the defence mechanism in mammalian that will ultimately lead to improve the sperm longevity in female tract by adding inhibitor proteins. It will ensure the presence of

spermatozoa for the fertilization of oocytes. This study will help the AI industry to produced high quality semen with maximum production potential.

Vitrification of bovine oocytes: The cryopreservation of female gametes (oocytes) is not as successful as in male gamete (sperm) due to their biochemical and structural differences, yet protocols are being developed for the vitrification of bovine oocytes. The effect of packaging system and equilibration time on vitrified bovine oocytes was investigated. Batch freezing (>3 bovine oocytes in straw or cryotop) could be done instead of single oocytes. The data revealed as high as 40% (48% of control) vitrified oocytes can be successfully matured *in vitro*. This study will help to conserve the female genetic material and produce offspring especially from endangered species.

Create new phenotypic and genotypic information including identifying new sources of disease resistance, abiotic stress resistance, nutritional quality, and bioactive compounds, through characterization and evaluation of bioresource attributes

AFLP analysis of 900 plains rough fescue plants collected from 30 populations across the Canadian Prairies was completed. Data processing and analysis are in progress. Final project report will be generated and delivered to Parks Canada (collaborator). From this research, we developed a marker-based approach to interpolating individual genetic information from a sample of plants to the whole population and empirically demonstrated the effectiveness of this approach for mapping genetic distinctiveness within 6 fescue populations across the Canadian Prairies. This approach is expected to play an important role in management and conservation of plant populations at risk.

Sequencing of 76 Canadian hard red spring wheat cultivars at Lr21 locus was completed. DNA sequences of about 4000 bp representing the Canadian wheat cultivars were completely aligned. Different analyses of diversity are in progress.

AFLP analysis of 40 Chinese flax cultivars and exotic germplasm was performed in collaboration with a Chinese visiting scientist (Dr. M. Li). Analysis of AFLP data is still in progress. Significant research findings may be written up for scientific publication.

1440 progeny rows of six *Camelina sativa* populations were grown, harvested individually to evaluate variation in seed oil content (NIR analysis) and were scored for severity of Aster Yellows disease.

Protocols were developed to screen barley accessions for seedling resistance to net blotch and spot blotch diseases. Cultures of net blotch and spot blotch strains were obtained from AAFC Winnipeg, and the National Fungal Collection. These cultures were regenerated and initial applications of inoculum made to barley plants in the greenhouse.

Characterization of chickpea germplasm for resistance to the fungal pathogen *Ascochyta rabiei* (ascochyta blight): 12 chickpea lines were screened for resistance to 48 *A. rabiei* isolates from Canada, Syria, India and Spain; five lines were highly resistant (immune) to all isolates; two lines showed a quantitative level of resistance to all isolates (minor R genes); three lines showed specific host-pathogen interactions (major R genes); while two lines were susceptible to all isolates; this data provides evidence of both quantitative and qualitative resistance. Genetic linkage maps of SSR and SNP markers were developed for 3 RIL populations derived from different resistant lines, and highly significant quantitative trait loci (QTLs) contributing to ascochyta resistance were identified.

A characterization nursery for *Dalea* (native Canadian plant) was established with the aid of collaborators. The nursery consisted of 8 lines, 5 of which originated from the native plant collection of PGRC. The 5 accessions were: NCP 368 – *Dalea* sp.; NCP 556 *D. candidum*; NCP 558 *D. candidum*; NCP 585 *D. purpurea*; NCP 591 *D. purpurea*. The remaining 3 accessions were the threatened species *D. villosa* (DV1; DV2; DV5). *Psoralea*: The collection contains 12 Psoralea accessions. Three accessions were used in an outdoor germination bed trial established in 2005. Germination counts made during the summer found a mean germination rate of NCP 50 (*P. esculenta*) at 1.25% in 2006 and 14.8% in 2007. NCP 95 (*P. lancelota*) had a germination rate of 13.1% in 2006 and 0% in 2007 and NCP 90 (*P. argophylla*) had a rate of 5.9 % in both 2006 & 2007.

Breeding strategies based on random bred and pedigreed populations in combination with repeated mating of sires allows for no rise in inbreeding until all sires mate with each dam or dam group. This strategy safeguards against loss of genetic variation and mean performance. The approach has potential merit in maintaining genetic authenticity of endangered breed populations.

Complementing North American sheep breeds that lack the inherent potential for increased fecundity and milk yield with the Finnsheep and Romanov as well as the newly developed Arcott breeds in Canada demonstrated outstanding lamb and ewe productivity as well as milk yield in long term trials at the University of Minnesota.

To taxonomically determine viral bioresources a search of the NCBI GenBank Database for *Carlavirus* sequences was performed to develop a database of sequence data as a foundation from which broad-spectrum RT-PCR primers could be designed. The GenBank data were sorted and organized in a DNASTAR Lasergene 7 database. Complete genomes were separated from the multitude of partial genomes which were further sorted by the region of the genome they span. Complete genomes are used for primer design and partial genomes for primer validation and phylogenetic analysis.

GenBank sequence files with complete viral genomes were selected for primer design. These consisted of 19 individual sequences representing 11 species in the *Carlavirus* genus. They were organized by genes and/or regions. Coding regions were organized by the corresponding translated protein. Sets of all homologous sequences were compiled in the FASTA format and aligned using the ClustalX and/or ClustalW algorithms. A primer set was used extensively to discover and collect information on new strains of the *Carlavirus*, Blueberry scorch virus (BlScV), which has been causing economic losses in the blueberry industry of BC. The virus is unusual as significant genetic diversity exists among the isolates examined from BC. The Carla–ORF2-3-F/Boeanchor primer set worked well in detecting all strains of the virus and of giving easily detectable RT-PCR results directly from blueberry plant extracts.

Assess genetic diversity changes in domesticated plant and animal germplasm

Analysis of genetic diversity in Sable Island horses was completed. Several North American horse breeds associations have shown interest in developing collaborative agreements to further characterize the genetic diversity within and between several horse breeds registered in Canada and the USA.

Initiated a genetic diversity study in Canadian pig breeds and commercial lines, the Canadian swine industry is concerned about the possible erosion of genetic diversity in their breeding stocks. Good relationships exist with breeders of minor pig breeds (Tamworth and Large Black) in collecting pig bristles for molecular characterization.

Research proposals to 11 major dairy and beef cattle breeds registered in Canada were submitted. The objectives are to monitor temporal changes in genetic diversity from genealogical records and multiloci DNA-based markers. Complete databases of pedigrees and DNA profiles from the Canadian Angus Association, the Canadian Limousin Association

and the Canadian Simmental Association have been received. Holstein Association of Canada has approved the research. The Canadian Hereford Association, the Canadian Charolais Association and the Canadian Maine-Anjou Association are waiting final approvals from their respective Board of Directors. Seven American beef and dairy breeds came forward and requested proposals for consideration by their Board of Directors. Maxxam Analytics Inc, a major DNA-based service provider to 20 different beef and dairy cattle associations and horse breed associations in North America, has fully endorsed the research proposals and has committed to freely share their multiloci DNA-based genotypes with CAGR.

Improving the structure of the GRIN-CA database for delivery of bioinformation

Plant genetic resource database

Considerable programming effort brought the GRIN-CA database into compliance with Government of Canada Common Look and Feel guidelines. Many front-end tables were updated for accuracy, completeness and link ability. Unfortunately CLF only makes use of about 2/3's of the width a full computer screen which results in an unattractive appearance for the GRIN-CA database. An initial database replication program was designed and is currently being tested for accuracy.

The GRIN-CA database was operational 365/24/7. No significant down time or computer malfunctions occurred. Since GRIN-CA became operational, over 20.5M hits have occurred and at a rate of over 14,000 requests / day made from over 120 countries.

Digital images of potato, large fruits and small grain accessions were added to GRIN-CA Passport data for clonal crops continued to be incorporated into GRIN-CA along with updates and corrections for many accessions. Characterization data was added for oat.

Animal genetic resource database

Development of an animal genetic resource database was initiated in cooperation with Brazil and the USDA (National Centre for Germplasm Preservation, Ft Collins). Discussions centred on content for 29 tables which ranged from inventory, taxonomy, donors, characterization and pedigree information, quality of donation, programming language, and hardware and software usage. Detailed programming is nearing completion, will be shared and integrated among the 3 countries. Windows XP and Unix Sun Solaris are being used

and the following software packages are being learned and utilized for database development: Oracle, MYSQL, Ruby, Ruby on Rails, JavaScript, Perl, PHP, TOAD, DBvisulizer, Oracle Form Builder, Oracle Database 10g Express Edition, Netbeans and Aptana Studio.

The current animal database includes three components: collection, repository and sample distribution. Sample collection contains sample donation and shipment information; the repository stores animal samples according to animal storage rules and procedures, and distribution reassigns current samples based on different requests (for research, evaluation, or working). Hierarchical structure was used in some tables to indicate the relationship between the upper-level and lower-level structure. The animal database was constructed on Oracle a RDM System and is in a Unix Sun Solaris server.

Contribute to access and benefit sharing regimens (acquire, donate, maintain, regenerate germplasm) consistent with Canadian commitments to international treaties, e.g. Convention on Biological Diversity (CBD) and the FAO International Treaty on Genetic Resources for Food and Agriculture (ITGRFA)

Germplasm from different sources was acquired. 361 samples from a joint Ukrainian-Canadian collection mission were completed. Wheat germplasm received from Bulgaria, Ukraine and the USA represented 164 accessions. Oat lines with a wide range of fat content (60 accessions) were obtained. Other acquisitions included: *B. napus*: 80 accessions **–** Nordic Gene Bank; 80 accessions **–** Czech Republic; 98 bean (*Phaseolus vulgaris*) **–** Ethiopia. The Clonal Repository acquired: four *Malus*, three *Prunus* and 21 *Fragaria* accessions. Two modern Canadian potato cultivars and five heirloom cultivars were added to the potato collection. 20 accessions were grown for agronomic evaluation, tuber glycoalkaloid analysis and plant, flower and tuber photographs in support of plant descriptions. One older cultivar and one heirloom cultivar were found to have glycoalkaloid levels above the threshold considered acceptable for human consumption.

Canada has signed and ratified the International Treaty on Plant Genetic Resources for Food and Agriculture. PGRC began using the Standard Material Transfer Agreement of the ITPGRFA in June 2008 which covers all plant germplasm held in Canadian collections. PGRC distributed germplasm within Canada and to 22 countries in 108 shipments. These shipments included 4850 accessions. About 49% of accessions were sent to Canadian clients, 33% sent to the USA and the remaining 18% to other countries. The Clonal

Repository distributed 607 accessions in 49 shipments involving 17,882 propagules. During the year 49 requests were received for potato accessions involving 552 clones. All but three requests came from Canada.

More than 65% of the PGRC collection is currently backup in safe secure duplication with the USDA at Ft. Collins, Co. In addition, PGRC sent about 6000 accessions, representing about 90 species to the Svalbard Global Crop Seed Vault in Norway as part of an international effort to safeguard global genetic resources. The Clonal Repository collected 2000 seeds from 2 *Prunus* accessions and 2000 seed from 400 *Malus* accessions for safe, duplicate back up at Saskatoon.

About 855 germination tests covering 20 genera were conducted. Over 31,000 germination tests conducted during 1998~2007 were entered into the GRIN-CA database.

For regeneration field plots, isolation sites, foliage tunnels (2) to increase heat units and prolong growth, greenhouse and growth cabinets are used. The following were increased in 2007: dry beans (39 accessions), faba beans (3), soybean (8), lettuce (4), Sorghum millet (7), *Pennisetum* millet (6), *Panicum* millet (1), buckwheat (1), egg plant (1), *Quinoa* (1) and sesame (8), mungbean (141 accessions), tobacco (2), wheat (141), sunflower (250), Jerusalem artichoke (358), cultivated flax (108), wild oat (436), cultivated oat (505), rye (87), barley (3500), wild barley (120), triticale (11), 45 accessions of *Poa alpina, P. arctica,* and *P. glauca* from the high Arctic and tomato (37), perennial oat, melons, coriander, cucumber, cantaloupe, pumpkin, winter squash, wild cucumber, *Echinacea,* buckwheat, bottle gourd, perennial flax, lupine and pea germplasm. About 60 alfalfa, 25 bird's-foot trefoil and 310 crucifer accessions were regenerated within pollinator excluded cages using leafcutter bees for pollination.

Detailed information about the PGRC lentil, chickpea, faba bean, grass pea, potato, barley, oat and wheat collections were compiled and provided to the Global Crop Diversity Trust, Rome for development of global plans for conservation of these crops.

Wild plant species surveys and seed collection in BC, Alberta, Saskatchewan and Manitoba included: a) 63 field days, 12,000 km of road travel, plant species surveys and seed collection from 71 locations; b) caging of native orchid species to prevent seed predation in collaboration with Manitoba Native Orchid Conservation; c) revision of the data collection form for seed collection; d) revision of a fact sheet on seed collection for

collaborators; and e) collection of 327 accessions of native plants (including seed from 41 uncommon or rare species) with data suitable for future use with GIS technology.

A Collaborative Agreement with Semex Alliance (world leader and provider of dairy cattle genetics and germplasm) was agreed. The CR calls for the transfer of about 200,000 straws of semen from close to 3000 dairy bulls to the CAGR germplasm collections. This represents a donation of approximately $5 M. It is anticipated that over the next 10 years, an additional 280,000 straws of semen will be transferred to CAGR representing another donation of $7 M.

Isolates of various *Carlavirus* species were obtained from other collections: (German) Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ). These isolates were revived from their storage state, as freeze-dried infected tissue, by preparing an inoculum and using it to infect herbaceous indicator plants. These were monitored for symptoms and were passaged serially to increase the virus titre as needed. Species specific RT-PCR primers sets were obtained for each virus either from literature searches or by designing sets based on available sequence data.

The Clonal Repository hosted the WERA20 2007 meeting. WERA deals with virus and virus like diseases of fruit trees, small fruit and grapevines nationally and internationally.

A senior undergraduate course in plant genetic conservation and utilization was offered by staff in the Plant Science Department, University of Saskatchewan. Animal genetic resource staff offered several lectures in animal science and conservation within the Animal/Poultry Science Department and the Western Veterinary College, University of Saskatchewan.

Other productivity: Peer reviewed scientific publications: 20; Presentations: 26; Posters: 12; Technical reports, abstracts, book reviews, book chapters, books: 39; Tours: 24; Exhibitions and demonstrations: six (especially potato); Training: three Post-docs, 2 Ph.D. students, five MSc students, numerous short visitors.

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Plant Genetic Resource Management in Indonesia

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Abstract

The loss of genetic resources which sustain people is now widely recognized to be critical; therefore, plant genetic resources have to be intensively managed. Plant genetic resource materials need to be conserved in crop research institutes as base and working collections. *Ex situ* conservation has been carried out with cold storage of seeds of plant genetic resources, while plant genetic resources propagated by vegetative organs are conserved in the field and *in vitro*. To increase public awareness, the National Committee of Genetic Resources promotes the importance of managing genetic resources. The morphological characters of plant genetic resources that have been collected in seed-field banks should be measured, and their resistance to biotic and abiotic stresses and their nutritional values should be evaluated. Germplasm accessions to develop core collections or for preliminary evaluations can be selected using cluster analysis involving quantitative plant characteristics. Plant genetic resources have been used as materials for agricultural research.

Introduction

Plant domestication began with the recognition and utilization of plant diversity by early farmers. This process occurred in various environments with diverse sets of native species which formed the foundation for the present diversity of agricultural crops. Further evolution occurred with the transfer of plant materials over wide areas, followed by their adaptation to differing local conditions. This process of recognizing and exploiting plant diversity for domestication continues to the present day and should remain an important element in crop preservation and adaptation to different environments.

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Indonesia is a country which has a large diversity of plant genetic resources. The loss of genetic resources which sustain people is now widely recognized as being critical. The endangerment or extinction of some species has occurred because of several factors including land uses, modern agriculture, availability of instant foods in the market, and people's consumption patterns. Modern agriculture is known to have caused erosion in diversity, especially inhabitants or landraces that have adapted to their ecosystems over long periods. Overexploitation of certain species and development activities disturbing habitats have caused the near extinction of certain species, which suggests the importance of *ex situ* conservation of such species (Moeljopawiro and Suprahtomo, 2007). It is essential that plant genetic resources be well conserved for use by present and future generations (Rao and Riley, 1994; Sastrapraja and Balakhrishna, 2002).

Plant genetic resources in Indonesia have been conserved by research institutes based on their national mandates, and this is coordinated by the Agency of Agricultural Research and Development (AARD). The collection, exploration, characterization, and evaluation of plant genetic resources have been consistently carried out. Plant genetic resources have been conserved mostly through *ex situ* conservation.

Institutions and regulations

Institutions intensively involved in managing plant genetic resources in Indonesia are mostly crop research institutes under the AARD, Ministry of Agriculture Research Institute managing plant genetic resources are listed in Table 1.

To increase public awareness, one of the activities conducted by the National Committee of Genetic Resources is to promote the importance of managing genetic resources in Indonesia. With increased public awareness, stakeholders should conserve the genetic resources in their area. Stakeholders can conduct conservation activities in their area with coordination of an institution, like a regional committee on genetic resources at the provincial level. It is important to coordinate the conservation of genetic resources at the national level by establishing a national network between the national committee and regional committees, because only with good coordination can well-planned conservation be conducted. Since 2001, the National Committee on Genetic Resources has encouraged genetic resource stakeholders at the provincial level to establish a network. As a result, to date, 17 regional committees have been established. One of the activities in networking was conducted at a congress of the Regional Committee on Genetic Resources in Balikpapan

(East Kalimantan Province) and a second congress in Pekanbaru, Riau Province (Nurhadi and Thohari, 2007).

Table 1. Research institutes managing plant genetic resources in Indonesia

1	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD)
2	Rice Research Institute (RRI)
3	Legume and Tuber Crops Research Institute (LTCRI)
4	Corn and other Cereals Research Institute (CCRI)
5	Ornamental Research Institute (ORI)
6	Vegetables Research Institute (VRI)
7	Fruit Research Institute (FRI)
8	Coconut and Palmae Research Institute (CPRI)
9	Citrus and Subtropical Fruit Research Institute (CSTFRI)
10	Center for Estate Crops Research Institute (CECRI)
11	Medicinal and Spice Crops Research Institute (MSCRI)
12	Oil Palm Research Institute (OPRI)
13	Tobacco and Fiber Crops Research Institute (TFCRI)

Legal norms in relation to policy and legislation may be sought within traditional systems, science, and technology as well as international conventions (Moeljopawiro and Suprahtomo, 2007). Indonesia has already ratified several conventions through Law no. 5 in 1994 for ratifying the United Nations Convention on Biological Diversity, Law no. 29 in 2000 for Plant Variety Protection, Law no. 21 in 2004 on the Ratification of the Cartagena Protocol on Biosafety to the Convention on Biological Diversity, and Law no. 4 in 2006 on the accession of the International Treaty on Plant Genetic Resources for Food and Agriculture.

Collection, conservation, and evaluation

Plant genetic resources include landraces, advanced/improved cultivars, and wild relatives of crop plants. Landraces which are distinct local types adapted to the many variants and interactions of natural and cultural environments are probably the most important among plant genetic resources (Rao and Riley, 1994). Exploration activities for collecting indigenous genetic materials have been done to protect and save these endangered species. Exploration has been done in almost every province but in only a part of the area due to budget limitations. The number of collections of plant genetic resources

resulting from exploration/collection and introduction of managing research institutes under AARD is presented in Table 2.

Table 2. Plant genetic resource collections under AARD, Ministry of Agriculture, Indonesia

Crops/Institute	No. of accessions
Cereals, legumes, and tuber crops (ICABIOGRAD)	10,563
Medicinal and spices-industrial (MSCRI, TFCR, and CPRI)	3590
Ornamentals (ORI)	961
Vegetables (VRI)	1507
Fruits (FRI and CSTFRI)	799
Estate crops (CECRI and OPRI)	
Coffee	1292
Cacao	570
Sugarcane	6009
Tea	870
Cinchona	600
Rubber	9130
Oil palm	7788

Organization abbreviations are defined in Table 1.

Ex situ conservation for seeds consists of cold storage, with seed viability being monitored yearly. *Ex situ* conservation of vegetatively propagated materials, such as tuber crops which are difficult to propagate by seed, is generally carried out in the field. *Ex situ* conservation of sweet potatoes, taro, and cassava has been done in the field and *in vitro*. Methods of *in vitro* conservation procedures have been applied to taro, sweet potato, and cassava germplasm. The following are the procedures of *in vitro* conservation that have been used for taro, sweet potato, and cassava (Nurwita, 2007).

Explants of taro were sterilized with 70% alcohol for 10 minutes, and 1.5% chlorine as a disinfectant for 10 minutes, and then grown in Murashige-Skoog (MS) medium for 2 months. Sterilized explants were grown in MS medium + 1 mg/l Benzyladenine (BA), and stored in MS medium + 4% mannitol for *in vitro* conservation.

Explants of sweet potato were sterilized with 70% alcohol for 5 minutes, 0.05% HgCl for 3 minutes, and 1% chlorine as a disinfectant for 5 minutes, and then grown in MS medium for 2 months. Sterilized explants were grown in MS medium + 1 mg/l BA, and stored in MS medium + 4% mannitol for *in vitro* conservation.

Explants of cassava were sterilized with 70% alcohol for 10 minutes, and 0.5% chlorine as a disinfectant for 5 minutes, and then grown in MS medium for 2 months. Sterilized explants were grown in MS medium + 0.1 mg/l gibberellins acid (GA) + 0.02 mg/l BA + 0.01 mg/l naphthalene acetic acid (NAA), and stored in MS medium + 0.1 mg/l GA + 0.02 mg/l BA + 0.01 mg/l NAA + 2% mannitol for *in vitro* conservation.

Conservation *in vitro* described above could be used for 10~18 months, and then crops have to be transferred to new medium to maintain their viability.

Morphological characters of most of the collection have been measured. Evaluations of plant characters observed mostly follow guidelines published by the IPGRI. Evaluation of plant genetic resources resistant to biotic (pests and diseases) and abiotic stresses (drought, iron toxicity, and acidic soils), and nutritional value have also been identified for several accessions of the germplasm collection.

Germplasm selection for the core collection

Germplasm accessions to develop a core collection or for preliminary evaluation can be selected using cluster analysis involving quantitative plant characteristics. The characteristics of a large number of accessions collected by research institutes holding plant genetic resources have to be evaluated. The genetic resources contained in germplasm collections are the basis for future progress in developing new varieties. Developing more-efficient methods for evaluating germplasm collections should help to speed up utilization of plant genetic resources. A core collection approach can be used to improve the efficiency of identifying valuable genes in germplasm collections (Corley et al., 2000).

Frankel (1984) proposed the core collection concept to denote a set which contains germplasm accessions with minimum repetitiveness, while retaining at the same time most of the genetic diversity of the principal collection. Characteristics of accessions selected in a core collection must represent the entire collection. The core collection can be determined based on qualitative and quantitative plant characters through cluster analysis. Cluster analysis is a technique of partitioning a set of accessions into clusters such that accessions within a cluster are homogeneous but are heterogeneous among clusters.

The number of groups or clusters can be determined by considering the percentage similarity, when the number of clusters is unknown. Accession samples can be obtained from each group using a constant or proportional strategy (van Hintum, 2000). The proportional

strategy allocates accessions to a group in proportion to the number of accessions in each group. The validation process usually involves comparisons between core collections and the entire collection.

Studies of germplasm accession selection for a core collection have been done for mungbean germplasm (Sutoro, 2008). Quantitative characters from 513 accessions used for the cluster analysis were flowering and harvesting times, branch number, seed number per pod, pod and seed numbers per plant, 100 seed weight, seed weight per plant, the ratio of seed weight to total dry matter, and plant height. Results of the correlation analysis among variables showed that several variables were significantly correlated. Euclidean distances used in the cluster analysis among variables were independent (Chatfied and Collins, 1980). All principal component scores were used as input variables for the cluster analysis.

Cluster analysis was performed using all principal component scores and considering 70% similarity. Results of the analysis showed that many clusters had only one member of an accession. In developing a method of defining a core collection, all of the populations sampled should be represented in the core, and as much of the diversity as possible from each population should be represented. Because all populations must be represented, each population will not necessary contribute to the core in the same proportion as it contributes to the entire collection (Skinner et al., 1999). For certain studies, genetic analysis with molecular or field evaluation of accession requires 96 samples for efficiency (electrophoresis requires 96 lines for running a molecular analysis). Distribution of accession numbers for each cluster can be determined but at least one member of an accession must be selected as a member of the core collection, while the rest can be allocated by a proportional strategy.

Samples can be validated by comparing the mean and variance of characters in the different groups of the core collection with those of groups from which they were derived (van Hintum *et al.*, 2000). A comparison between the core collection and the entire collection can be carried out using characteristics that were involved in establishing the core or using characteristics that were not used in its development.

To evaluate how well those 96 accessions of the core collection represent the entire collection, the mean and variance of each character in the core collection (accessions of which were selected at random) were compared with the corresponding mean and variance of the entire collection. Pairwise comparisons of the mean and variance of each trait indicated that most of the means and variances of the plant characters did not significantly differ between the core collection and entire collection. Correlations (data not shown) of

flowering time with branch number and seed weight significantly differed between the core collection and entire collection, but the directions were similar.

Development of the core collection is better when using molecular techniques, because they are not affected by environment factors, but molecular analyses are relatively costly.

Utilization of plant genetic resources

Numbers of accessions of plant genetic resources requested by researchers or students/universities during 2007 and 2008 were served by ICABIOGRAD as shown in Table 3. The recipients of plant genetic resources have to sign a material transfer agreement. The recipient agrees to use the materials for research purposes only, and not for any commercial use. Germplasm requested by a user generally has certain characters such as being susceptible, resistant, or tolerant to biotic and abiotic factors.

Table3. Numbers of accessions of plant genetic resources (germplasm) in ICABIOGRAD requested by researchers and students in 2007 and 2008

Crops	Number of accessions requested	
	2007	January~September 2008
Rice	154	29
Corn	10	6
Sorghum	5	-
Peanuts	27	-
Soybeans	200	28
Mungbean	42	12
Sweet potatoes	-	150

Utilization of plant genetic resources for commercial use by private companies to produce new varieties occurred in 2005. The local variety of peanuts belonging to a farmer group was used as a source of genetic material to obtain a new variety. These local varieties were registered with the Plant Protection Variety Office, Ministry of Agriculture. Negotiations between farmers and the company were mediated by the local government to obtain benefits for using local varieties. As a result of the negotiations, the farmers received a budget from the company for their input production, such as tractors and other facilities.

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The Present Status and Future Prospects of the NIAS Genebank Project in Japan

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Abstract

Since 1985 the National Institute of Agrobiological Sciences (NIAS) has coordinated a national genebank project in Japan that has focused on conservation of plant, microorganism and animal genetic resources related to agriculture. More recently DNA materials have been added to the project. NIAS has also established a Rice Genome Resources Center. Central to the efficient working of the genebank project has been the database system that now includes illustrated databases and marker databases. Research to develop core collections for various crop species has progress recently and germplasm users are requesting these germplasm research sets. Future challenges including continuously incorporating new technologies to improve efficiency, cost effectiveness and usefulness of genebank materials and operations. International cooperation is a key component of Japan's strategy to ensure global safety and exchange of conserved genetic resources. Key to the future of the national and global genetic resources system will be realizing and recognition of the usefulness of genetic resources to sustaining and improve agricultural productivity.

Introduction

The Ministry of Agriculture, Forestry and Fisheries (MAFF) of Japan initiated the genebank project in 1985 to focus on conservation of genetic resources related to food and agriculture. The National Institute of Agrobiological Sciences (NIAS) has functioned as the "center-bank" for genetic resources of plants, microorganisms, and animal for food and agriculture in cooperation with "sub-banks" or agricultural research institutions across Japan. The center-bank at NIAS is responsible for the coordination of the project, planning and implementation of domestic and international activities. The NIAS Genebank project

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activities encompass collection, conservation, characterization and distribution of genetic resources including agricultural plants, microorganisms and domesticated animals. In the 1990's it became apparent that DNA was a necessary component of the center-bank at NIAS to reflect progress in plant genomics and genome informatics and this aspect became incorporated into the genebank project. In 2003 a new center was established the Rice Genome Resources Center to provide retro-transposon-mediated insertion mutant lines of rice, useful rice experimental materials for genetic analysis such as recombinant inbred lines, and full-length rice cDNA clones, and rice genome information and analytic tools. Now NIAS has a genebank that coordinates plant, animal, microorganism and DNA genetic resources related to food and agriculture and a Rice Genome Resources Center.

Present status on plant genetic resources for food and agriculture (PGRFA) in the NIAS Genebank project

The Plant Section of the NIAS Genebank project conducts exploration, collection, characterization, evaluation, preservation, multiplication, and distribution services of PGRFA for traditional landraces, improved cultivars, breeding lines, and to some extent wild relatives to fulfill expanding demands of plant breeders and research scientists.

The plant collections conserved in NIAS genebank are included in the following 13 groups (Number of accessions as in 2008);

* Rice (44,224),
* Wheat and barley (62,333),
* Legumes (18,956),
* Root and tuber crops (8,889),
* Millets, other cereals, industrial crops (19,058),
* Grasses and forage crops (33,099),
* Fruit trees (10,300),
* Vegetables (27,224),
* Ornamental flowers and trees (5,873),
* Tea (7,547),
* Mulberry (2,178),
* Tropical and subtropical crops (418), and
* Others, such as herbs and spices (3,364).

The Plant Section has been dispatching both domestic and overseas exploration teams annually to survey the distribution and collect the variation of plants. The total number of newly registered PGRFA amounts to over 5,000 accessions per year, including accessions obtained by exchanges with domestic and overseas research institutes. Activities of such exploration missions can be viewed in the Annual Report on Exploration and Introduction of PGRFA at:
http://www.gene.affrc.go.jp/publications.php?section=plant&type=report.

Collected plants are identified, characterized and analyzed by researchers. Cultivation for seed multiplication is conducted at the same time. The harvested seeds are preserved in a low-temperature and low-moisture environment over the long term. The number of registered accessions is over 240,000 as of 2008.

The information on the history and properties of the registered genetic resources is added to the database and is made open to the public through the Internet. The database can be searched by property, and information on any genetic resource with the desired properties can easily be obtained at:
http://www.gene.affrc.go.jp/plant/SEARCH/db/index-e.html.

The genetic resources preserved at the NIAS Genebank can be requested for testing/research or educational purposes. Annually 5,000~10,000 accessions are distributed to both domestic and overseas research institutes, contributing to research and development. Materials from the genebank are used in analyses of genetic, physiological, ecological diversity, plant breeding and as possible raw materials for food processing. Our PGRFA are expected to bring about major developments in agriculture and agricultural science through breeding programs and other procedures as exemplified by “Nipponbare” whose whole genome information was analyzed by scientists mainly based at NIAS and by “Wataribune”, an old cultivar that has been underutilized but is now used as brewing rice.

Among the total of over 240,000 accessions, the NIAS center-bank conserves 156,909 accessions of which 112,015 are in the active collection. The remaining PGRFA are preserved at sub-banks. As the center-bank of the project, NIAS has two seed conservation facilities; one for long-term conservation (base collection) and another for distribution (active collection). The former is kept at –10 ºC and 30% RH, while the latter at –1 ºC and 30% RH. Each accession registered in the NIAS Genebank system is grown for multiplication and characterization, and the seed is gently dried at room temperature and preserved in the two storage facilities. The seed germinability is tested once every five-year, accessions with

germination below a set threshold or with few seeds are multiplied from the seed samples preserved at the long-term conservation facility.

Domestic and international collaborative field surveys and exploration missions are organized by the Project. Routine characterization for primary characters (basic morphological and ecological characters), secondary characters (stress tolerance) and tertiary characters (crop quality characters) are investigated mainly by specialists in sub-banks according to Japanese descriptor lists. In 2007 data items totaling 120,000 (no. of accessions x characters) were recorded for primary characters, 25,000 for secondary ones, and 29,000 for tertiary characters. In addition, new characterization trials, pre-breeding or genetic enhancement, and selection of core collection or special germplasm research sets of genetic diversity are supported by the genebank project based on research proposals. Examples of recent research of genebank project scientists related to core collections can be found in the following publications: Kojima *et al*., 2005 in rice; Sangiri *et al*. 2007 in mungbean; and Xu *et al*. 2008 in azuki bean. About 5000 PGRFA accessions are multiplied annually for seed crops. Cryopreservation has successfully been performed for about 1500 mulberry accessions. Research is currently being conducted to improved cryopreservation technology for different PGRFA such as Chrysanthemum and Juncus species.

The NIAS genebank project intends to expand the active collection that is available for users. After the CBD came into effect in 1993, the genebank project has been careful regarding sovereign rights and intellectual property rights on PGRFA, since our policy is compliance, accountability and ethics. For that reason we have precisely examined each accession regarding status. We are striving to ensure whole information of accessions conserved in the NIAS Genebank is available and all collections are able to distribute for requester.

The NIAS Genebank has the responsibility to distribute the PGR for breeding, research, and educational purposes to the breeders and scientists of research institutions in Japan and international request. For scientists who are interested in germplasm related to food and agriculture within the NIAS Genebank system, they are directed to the databases that provide full details of how to request materials in each category of genetic resource. The databases including information on passport data, evaluation as well as more general information on genetic resources in the NIAS Genebank that can be found at this web site at: *http://www.gene.affrc.go.jp/databases_en.php*.

Future prospect of the NIAS Genebank in relation with international research cooperation

Japanese scientists are eager to establish cooperative linkages and exchange genetic resources with other countries.

International relations of the NIAS Genebank project

The NIAS Genebank actively participates in collaborative activities with other countries in relation to surveys and research related to agricultural related genetic resources. In all activities related to conservation of genetic resources the NIAS Genebank follows the international community norms and national regulations. Plant and microorganism germplasm within the NIAS Genebank system collected in Japan is available for research purposes.

In addition to exchanges of PGRFA and their information, four different kinds of international cooperation program are incorporated into the NIAS Genebank project – joint explorations, a cooperative research programs especially related to *in situ* conservation of PGRFA with developing countries, overseas multiplication and evaluation of PGRFA, and international workshops on PGRFA.

Approximately four missions are dispatched overseas annually to conduct exploration and collection of PGRFA in collaboration with scientists in other countries. The plant materials collected in each country are always divided into two sets: one set is transferred to Japan based on the material transfer agreement (MTA) between Japan and the country and another set is conserved in the country. The duplication of conserved genetic resources is beneficial to researchers of both countries. This has always been the practice since the beginning of the NIAS Genebank project. Such joint exploration enhances conservation and understanding of PGRFA, increases mutual understanding and provides a basis for further research cooperation.

Regarding the conservation of wild species, it is often difficult to preserve their diversity *ex situ* within a genebank and *in situ* conservation is necessary. The project of NIAS Genebank is consisting of a special program to encourage researchers in developing countries to survey the status of populations in the field and monitor them in cooperation with Japanese scientists at the sites as well as analysis of the populations by molecular

techniques at NIAS and other related institutions. This reciprocal approach helps *in situ* conservation of PGRFA, especially wild relatives of cultivated plants, and also assists capacity building of researchers in collaborating countries. *In situ* conservation research activities of the NIAS on wild legumes and wild rice were started in collaboration with the Plant Genetic Resource Centre (PGRC) of Sri Lanka in 2000. Japanese researchers joined the missions in Sri Lanka to monitoring genetic structure of wild *Vigna* species and wild *Oryza* species. While Sri Lankan researchers who participated in the program could learn various molecular techniques in Japan as well as join collecting missions in Japan (Jayasuriya and Vaughan, 2003). An *in situ* conservation project on *Fagopyrum* species sponsored by Bioversity International (then IPGRI) was conducted in Nepal from 1999 to 2001 in a similar manner. Genetic diversity of the wild species *F. cymosum* successfully identified the populations most suitable for *in situ* conservation of this species. Indonesian and Korean researchers have participated in a similar program on sweet potato (*Ipomoea batatas*) and *Perilla* species, respectively.

An overseas multiplication and evaluation program has been initiated to ensure sufficient quantity of quality seeds for the secure conservation of PGRFA in the NIAS Genebank, since it is difficult to grow certain crop species under the climatic conditions of Japan. Japan and the collaborating country can share both the multiplied seeds and obtained characterization and evaluation data. For example, wheat and barley genetic resources are being multiplied and evaluated in cooperation with scientists at the Vavilov Institute of Plant Industry, Russia, and soybean and other food legumes genetic resources are being multiplied and evaluated in Thailand.

International workshops on PGRFA serve as a good opportunity for researchers worldwide to exchange up-to-date information and to initiate future research cooperation. For example, the International Genetic Resources Workshop supported by the genebank project of Japan titled as “The Genus *Oryza*” was held at Tsukuba from 24th to 26th September, 2003 at NIAS. In 2006, an international symposium supported by the genebank project and OECD on crop domestication and super-domestication was held in Tsukuba (Annals of Botany Special Issue in October, 2007).

International cooperation on PGRFA through JICA projects

The Japan International Cooperation Agency (JICA) has implemented a series of grants-in-aid and technical cooperation projects as official development aid (ODA) of Japan

in relation to PGRFA. It contributed to the establishment of genebanks in Sri Lanka, Chile, Pakistan, and Myanmar as well as scientific capacity building. As the responsible institute on PGRFA in Japan, NIAS has always participated in feasibility studies at project sites, the detailed project planning, and research coordination for smooth implementation and fruitful achievements of the JICA undertakings.

For example, construction of a Seed Bank and a technical cooperation project was planned based on collaboration between Japan and Myanmar under a scheme of JICA to collect, evaluate, and conserve agricultural PGRFA in Myanmar and to promote their use in breeding programs. The Myanmar Seed Bank was created within the Central Agriculture Research Institute (CARI) at Yezin in 1990, and a technical cooperation project was implemented as “Myanmar Seed Bank Project” from 1997 to 2002. The project objective was to develop the Seed Bank into a sustainable national genebank, and Myanmar staff and Japanese experts collaborated well to set up and improve the PGRFA management system suited to the conditions of Myanmar.

During such technical cooperation projects, long-term and short-term experts are dispatched from Japan. They make suggestions to improve the management of genebanks, supervise the research activities on genetic resources and conducted cooperative research. Young researchers in the country are invited as trainees to a 6-month JICA sponsored group-training course on genetic resources held annually based at NIAS or to an individual training course to study various aspects of genetic resources in Japan. A few excellent young researchers from a project site can apply for a MONBUKAGAKUSHO (MEXT) Scholarship to study PGRFA and related research fields at some universities in Japan.

Cooperation with the international framework

The Bioversity International (previous IBPGR, later IPGRI) is the world’s largest non-profit agricultural research and training organization devoted solely to the study and promotion of agricultural biodiversity. The Government of Japan started assistance to the Bioversity International in 1979, and has been one of the main financial supporters since 1987. Japan also supported several international projects organized by Bioversity International. The NIAS Genebank was assigned by Bioversity International to be the global base genebank for Japonica cultivar group of rice.

Japanese scientists have been dispatched to carry out collaborative exploration for PGRFA in Nepal, Pakistan, Vietnam, Mongolia and other countries based on the special

funds provided by the Ministry of Foreign Affairs (MOFA) of Japan to Bioversity International. The materials collected were divided into three sets for conservation by the countries explored, Japan, and Bioversity International.

Bioversity International and Japanese agricultural research institutes have cooperated for holding international meetings. For example, the NIAS cooperated with Bioversity International in holding international symposia on several underutilized crop genetic resources (e.g. IBPGR, 1992). The Japan International Research Center for Agricultural Sciences (JIRCAS) and Bioversity International co-sponsored an international symposium on Cryopreservation of Tropical Plant Germplasm, held in Tsukuba (Engelmann and Takagi, 2000).

Future perspectives from Japan on international relations and PGRFA operations

Japan is generally considered to be a gene-poor country. However, it was germplasm developed in Japan, Norin 10, which provided vital genes for the green revolution in wheat. This illustrates that so-called gene-rich and gene-poor countries depends very much on what you are looking for in germplasm.

Japan has been an active partner in all the major international developments related to PGRFA and biodiversity. The CBD will meet in Nagoya in 2010. The global consensus related to PGRFA is changing. An International Treaty on PGRFA came into force in 2004. A Trust Fund to assist sustainable conservation of PGRFA is now established. Japan will continue to be an active partner in these international activities related to PGRFA and biodiversity in the future.

Japan has established strong collaborative relationships with many countries over the past decades in relation to PGRFA. Japan seeks to extend these linkages to other countries by helping capacity building and importantly understanding plant genetic resources and developing safe sustainable means of their conservation.

The future challenges include sustaining concern for the never-ending job of PGRFA conservation that means countering funding fatigue. To sustain funding for genebank operations it is necessary to be proactive in explaining that efficient and effective genebanks are the foundation upon which future agricultural development and thus food security depends. It is also necessary that genebanks evolve quickly to keep up with technological developments to improve all aspects of genebank operations. For example, genebanks will

need to become “green” as costs of maintaining cold storage facilities increases. In addition, genebanks are challenged to use research tools and new approaches to find within our germplasm collections the new superstar accessions like Norin 10. The future of the genebanks ultimately rests on providing high quality of service to users particularly plant breeders.

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Status and Progress of Conservation and Utilization of Agricultural Genetic Resources in the Republic of Korea

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Abstract

The RDA Genebank project has been implemented as a national program in Rep. of Korea to collect, characterize, evaluate, rejuvenate, conserve and use plant, microorganism and animal genetic resources for food and agriculture since 1985. National Agrobiodivresity Center (NAC) has functioned as a central bank of the project in cooperation with other agricultural public and private sectors. This national network on genetic resources for food and agriculture currently preserves approximately 154,695 accessions of crops germplasm and wild relatives as the base collection of about 1700 species involving 26,125 accessions of clonal crops. About 100,000 accessions are conserved as active collection, which are able to distribute mainly for breeding and research purposes under the regulation of MTA between RDA Genebank and recipients worldwide. We have undertaken international collaboration with several Asian countries focusing on *ex situ* conservation of plant genetic resources. Research highlights on conservation and utilization of plant genetic resources are discussed.

Introduction

The RDA (Rural Development Administration) plays a key role in planning and supporting the national program on conservation and use of crop genetic resources. RDA Genebank (RDAGB) was established in 1988 and organized as a National Agrobiodivresity Center (NAC) of RDA on 3 November, 2006 of the completion of the new bank facilities. The genebank projects undertake research on germplasm collection, characterization, evaluation, conservation and documentation for future use. The Genetic Resources Council (GRC) and the Germplasm Advisory Committee (GAC) advise RDA with establishment of national strategies for Plant Genetic Resources (PGR) activities such as priority settings for collecting,

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and making recommendations to carry out characterization, evaluation, and utilization of PGR throughout the nation. Evaluation and regeneration of the PGRs are conducted jointly with other related research institutions. The seeds multiplication and the data evaluation at those related institutions are sent back to RDAGB for conservation and utilization.

The RDAGB's effort has been focused on the collection, conservation, and utilization of PGRs for using in research for crop improvement and other utilizations. Research infrastructure of PGR is very important in order to improve and utilize the collections. However, there are numerous problems encountered in the conservation and utilization of PGR in Korea. Also, social understanding and consensus (i.e. public awareness) on the important issues of genetic diversity or PGR are needed urgently. For realizing further development of food and agriculture and for achieving three objectives of the CBD, the RDAGB pursues the proposed activities for implementing Global Plan of Action (GPA) adopted by the International Technical Conference on Plant Genetic Resources in Leipzig, 1996 (FAO, 1996).

The conservation and utilization of PGRs need a long-term plan at the national and international level. Further efforts are required to develop additional databases for germplasm including additional image data, DNA profiles, and molecular characterization. The RDAGB has started the conservation of mutant and genetic stocks for genomic and functional researches. For upgrading characterization and evaluation data of PGRs through using genetic and biochemical tools including gene expression displays such as DNA microarray data has to be involved in the program of PGRs in the Republic of Korea.

In situ management of agro-biodiversity

The RDAGB has surveyed the distribution of some wild relatives of crop species and the diversity assessment of weedy type found in farmers' lands. The wild adzuki bean (*V. angularis* var. *nipponesis*) is a progenitor of the cultivated type (*V. angularis* var. *angularis*) and *V. nakashimae* is a wild relative (Fig. 1). Both two wild species are distributed in the whole regions of the Korean peninsula. The survey on the distribution of the wild adzuki bean and its relative species, *V. nakashimae,* has been conducted in the basins of 'Taebaek' and 'Jindo' in Korea. Seeds of 165 accessions were sampled for planting for further characterization in 2002. The RDAGB preserves about 1,000 accessions of wild soybean, which were collected during 1991-1995. The supplemental surveying on the wild soybean was implemented for the *in situ* management of crop wild species (Fig. 1).

The weedy rice was surveyed across the different regions based on the five rivers, Hangang, Geumgang, Nakdonggang, Yeongsangang, and Seomjingang. A total of 3599 accessions including collections from Jeju island were sampled from nine provinces and it had been done in 2002. These collections are complementary one for the previous weedy collections made by Dr. Suh in the Yeongnam University. These accessions were re-evaluated by comparative analysis based on phenotypic and DNA analysis during 2004-2005. The duplication and on-farm conservation status should be fully understood by the following study.

Wild *Vigna* Weedy Rice

Fig. 1. The comparison of seeds in *Vigna angularis* and *V. nakashimae* (left), and the characteristics of plant and spike type of weedy rice (right).

The surveys have been conducted over several years (Ahn *et al*. 1994). The result shown the crop landraces disappeared very fast from the farms in Korea. Only 26% of the various crop landraces could be found according to the survey in three locations in South Korea in 1993 relative to 1985. A similar trend could be expected in other rapidly developing countries. One of the main reasons for the genetic erosion of landraces is their rapid replacement by a much narrower spectrum of bred cultivars improved cultivars. Other reasons are the simplified cropping systems and young people migration into city due to mechanization of agricultural system. The status of landraces maintained on farms at different geographic locations in South Korea was investigated in 1985, 1993, and 2000. Therefore, 274 farms were established in the remote mountainous areas such as ‘Pyungchang’ and ‘Youngduk’ in 1985. However, the number of farms was eventually reduced to 44 (16.1%) in 2000. The numbers of farms were reduced from 170 to 18 (10.6%) in sub mountainous areas,

from 537 to 65 (12.1%) in plain cultivating areas, 463 to 66 (6.6%) in suburb areas and from 34 to 1 (2.9%) in Jeju Island. Jeju Island is the biggest island in Korea. Thus, 1478 farms held landraces in 1985, in which 194 (13.1%) farms were still cultivating at least one landrace in 2000. It is a general tendency that farming areas near to cities would lose crop landraces resulting from changing to new commercial cultivars. According to the species diversity is based on the number of crop species kept by farms, the relative retained proportions of crop species appeared to be 29.3%, 35.5%, 28.6%, and 4.5%, respectively, in different farming areas in 2000, compared to that of 1985. With average, about 28.2% of crop species were maintained in 2000 *versus* in 1985. More diversity of crop species was cultivated in the plain and rural farming areas rather than the remote mountainous farming areas. In general, the total number of varieties hold by farms has been also drastically decreased. The number of varieties in remote mountainous areas was relatively higher than that of other areas.

The industrialization of agriculture led farmers to change their traditional varieties to new-bred ones or simplify diverse varieties into one or a few. About 35% farmers were holding landraces because of high quality (35%), 34% because of importance of heritage for home consumption while 31% for other preferred reasons (Fig. 2). On the other hand several reasons were also identified which forced the farmers to avoid use of landraces. Among these, 25% for farmers having no land anymore as they moved to cities, 23% for quitting farming, 9% for shifting to new varieties, 17% for cheap prices relative to new varieties, 19% for lack of labour, and 7% for unknown reasons.

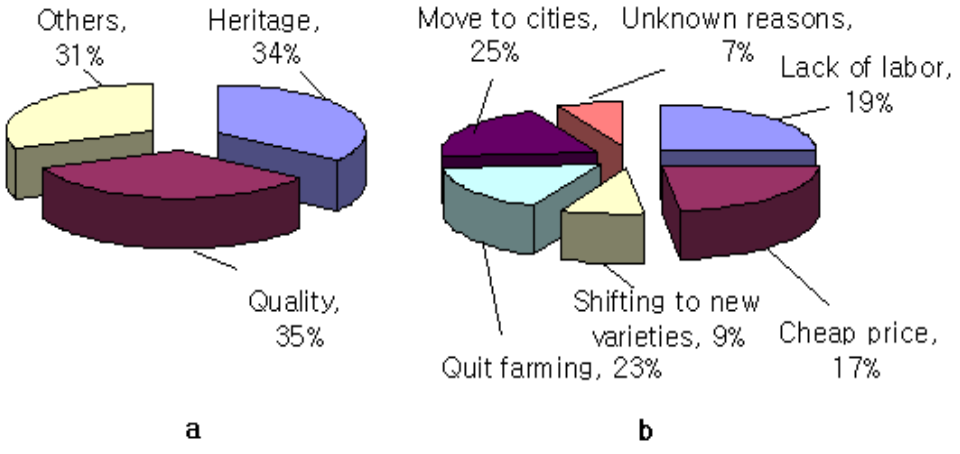


Fig. 2. The preference and avoidance for cultivating landraces in farms in Korea.

Ex situ conservation

Wild relatives of crop species have potential uses in improving agronomic characters and disease resistances. The major wild relatives in RDAGB are wild soybean (950 accessions), medicinal plants (714 accessions) and *Allium* species (1466 accessions). During last three years, the 1304 wild *Raphanus* accessions were collected from Jeju Island and southern coastal regions in Republic of Korea. As for the wild *Vigna* collection, the 76 accessions of wild adzuki bean, 88 *V. nakashimae* and one weedy type of *V. angularis* were collected in the regions of Taebaek and Jindo. In total 3,599 accessions of weedy rice from farmers' fields were collected for a case study for the diversity maintained in on-farm status before Genetically Modified Organisms (GMO) releasing (Table 1).

Table 1. The status of domestic collection of weedy rice (2002~2003)

Sources	Gyeonggi	Gangwon	Chungcheong	Jeolla	Gyeongsang	Jeju	Total
No. of accessions	298	218	1005	807	508	763	3599

Seed storage facilities of the RDAGB were built newly last November, 2006 according to the international standards set by the International Plant Genetic Resources Institute (IPGRI) and the Food and Agricultural Organization (FAO) of the United Nations. It has the capacity to store as many as 500,000 accessions with its medium-and long-term seed storage rooms, respectively (Table 2). The 264 m^2 long-term storage room is set at the condition of –18±1 ^oC temperature with 40% relative humidity (RH). The 674 m^2 mid-term storage room is set at 4±1 ^oC temperature with 30% relative humidity (RH). Seeds are dried to 3% to 8% moisture content prior to their storage. Packing room is set at 20±3 ^oC and 30% RH. In addition, a few national as well as private research institutes have short-term storage facilities where temperature is maintained at 5 ^oC to 12 ^oC.

Seeds to be stored for a long term are packed in aluminium foil bags, dehydrated and kept in –18 ^oC storage room, while the seeds for medium-term storage are packed into a PET bottle with silica-gel and kept in 4 ^oC storage room. The duplicated collections are kept at the National Yeongnam Agricultural Institute under National Institute of Crop Science for safety purpose.

Table 2. Preservation facilities and preserved accessions of RDAGB (2007)

Facility	Condition & area	Practical duration & capacity	Preserved accessions	Type of germplasm
Long-term	–18°C, 40% RH 264 m^2	> 100 years 500 x10^3 Acc.	86,373	Seeds
Medium-term	4°C, 30% RH 674 m^2	> 10 years 500 x10^3 Acc.	10,000 154,695	Mutants Seeds
Field Genebank	Field & greenhouse	1~50 years	26,175	Vegetatively propagated materials

The accessions after collection and introduction are submitted for tagging with temporary storage numbers. Basically, new accessions need primary multiplication and characterization for permanent storage. All the passport data and related characterization details are databased. Curators of corresponding PGR are charged with the management of related activities through the entire process. RDAGB takes IT (Introduction) No. for permanent storage and has a temporary storage number system for new accessions.

RDA seed genebank conserves 117,275 accessions of cereal crops, 18,617 of industrial and medicinal plants, 14,984 of vegetables and fruit trees and 3,819 of forage crops and other germplasm, collected within the country and abroad (Table 3). With respect to the vegetatively propagated germplasm, 45 field gene-banks maintain 26,175 accessions consisting of fruit trees, flowers, vegetables, medicinal plants, tuber crops, shrubs, grasses, and other germplasm (Table 4). As mentioned above, the RDAGB has started a systematic conservation of mutants for genomic researches since 2003. Basically, the RDAGB plays long-term conservation of mutants. Active collections are operated by each university or institute, which had developed each mutant population. Around 10,000 accessions of mutants are kept in long-term storage for safe conservation of these mutants now.

Developing and adopting *in vitro* conservation system for recalcitrant seeds and vegetatively propagated PGRs is also a major research program of RDAGB. The experiment for optimizing conditions for ultra low temperature using liquid nitrogen is being undertaken for potato, tea and garlic genetic resources (Kim *et al*. 2002; 2004). In the cryopreservation of potato *in vitro* shoot tips, stepwise increase of sucrose from 0.3M to 0.8M in pre-culture medium resulted in the highest survival. Dehydration with PVS3 solution for 90 minutes or

PVS2 + PVS3 solution for 60 minutes showed higher survival than with other solutions tested. Primary shoot tips only showed high survival to cryo-exposure in pre-culture for three or five weeks, while middle part shoot tips showed a high survival in pre-culture for six or eight weeks.

Table 3. Germplasm collections in the RDAGB (~2007)

Crops	Number of species	Number of accessions	Ratio (%)
Cereal crops	414	117,275	75.8
Industrial & medicinal plants	258	18,617	12.1
Vegetables & fruit trees	462	14,984	9.6
Forage crops & others	643	3,819	2.5
Total	1777	154,695	100.0

Table 4. Collections of vegetatively propagating plants in the RDAGB (~2007)

Crops	Number of accessions
Fruit trees	7,962
Vegetables	2,500
Ornamental plants	5,403
Others	10,310
Total	26,175

The droplet-vitrification protocol was applied to unripe inflorescences of plants of four Korean garlic field collections at Danyang, Suwon, Mokpo and Namhae, to establish a cryopreserved germplasm collection. The protocol applied was consisted of preculture for 3~5 days at 10°C on solid MS medium with 0.3 M sucrose, loading for 40 min in liquid medium with 35% PVS3, dehydration with PVS3 vitrification solution for 150 min, cooling in 5 µl droplets of PVS3 vitrification solution placed on aluminum foil strips by dipping these strips in liquid nitrogen, warming them by plunging the foil strips into pre-heated (40°C) 0.8 M sucrose solution for 30 s and further incubation in the same solution for 40 min (Fig. 3). A total of over 800 accessions of five clonal *Allium* species, including garlic, were stored in liquid nitrogen for long-term conservation using unripe inflorescences, cloves or bulbils. In addition to *Allium* species, currently 93 accessions of potato and 560 accessions of Korean ginseng seeds were stored in liquid nitrogen for cryopreservation.

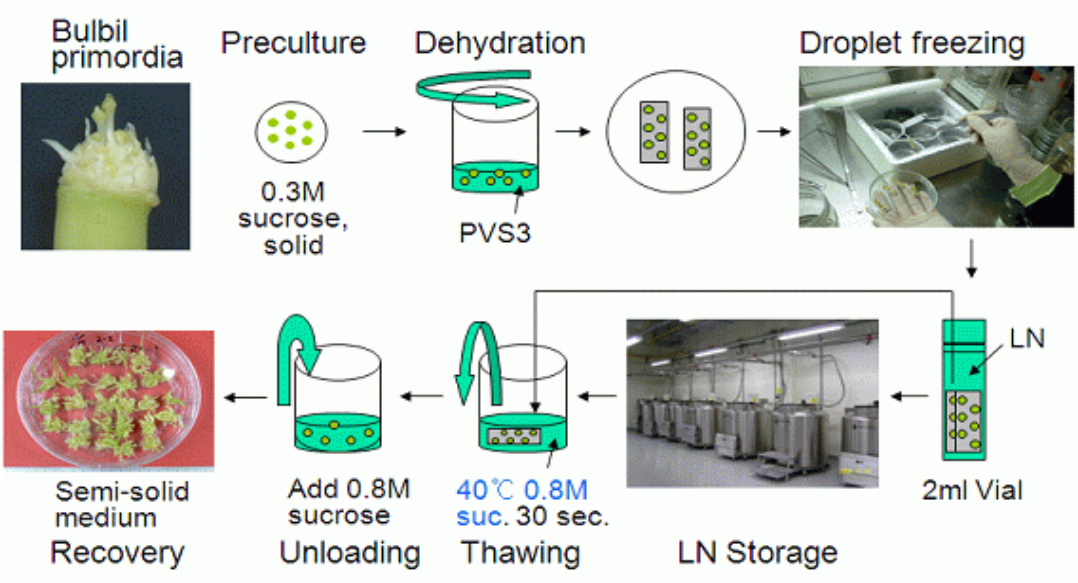


Fig. 3. Cryopreservation protocol for garlic unripe inflorescences by droplet-vitrification procedure.

The RDAGB is developing a DNA Bank for the accessions, focused on Korean originated landrace. So far, the DNA stocks of 15,000 accessions have been established and kept in –20 ^{o}C at the refrigerators. After developing DNA profile with the molecular markers, the data will be distributed to the researchers of the RDA institutes for mining of genes related to important traits.

Utilization of genetic diversity

Characterization and evaluation data may help researchers to search for desired combinations of traits and request to the RDAGB for the supply of appropriate seed samples. Characterization and evaluation of the stored germplasm samples are carried out by scientists working both in RDAGB and various crop experiment stations of RDA. The RDA descriptors were developed by partially modifying the IBPGR/IPGRI descriptions. About 75% of the stored germplasm by RDAGB has been characterized by 2007, and evaluated for various traits including physiological responses, disease and pest susceptibility, yield productivity, and other agronomic features (Table 5). The national project on regeneration and characterization is progressing well in collaboration with all the institutes under the RDA. By

2007, 115,999 accessions have been regenerated and characterized. In 1991, the RDAGB was designated as the centre of world sesame germplasm collections by FAO and IPGRI, and since then 1,600 accessions of sesame have been characterized and evaluated.

Table 5. Characterization status of germplasm preserved in the RDAGB (~2007)

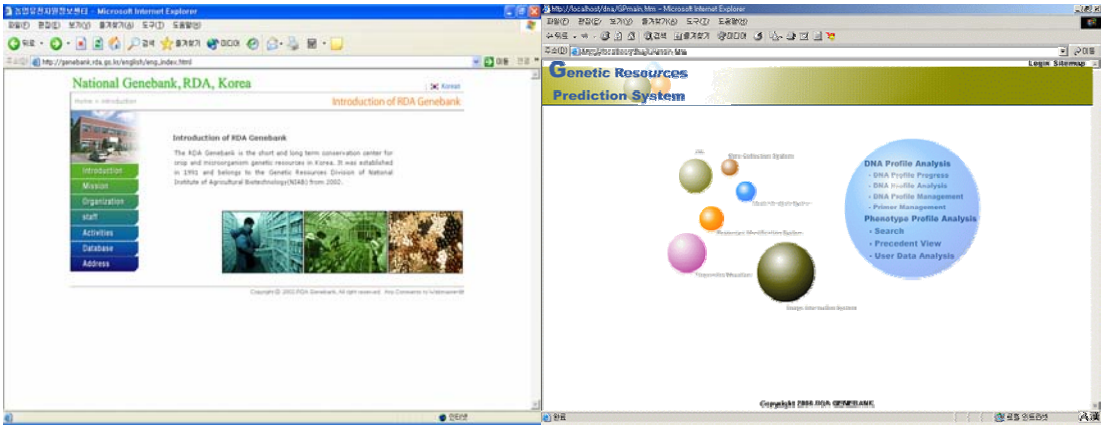
Crops	No. of preserved accessions	No. of characterized accessions	Ratio (%)
Cereals	117,275	94,011	80.1
Industrial & medicinal plants	18,617	11,656	62.6
Vegetables	14,984	8,365	55.8
Others	3,819	1,967	51.5
Total	154,695	115,999	74.9

* The RDAGB did not count the rate of characterized accessions since 2002 because different crops have been scored by different numbers of descriptors.

Information and capacity building

The information of germplasm preserved in RDAGB consists of passport, seed stock, characterization, evaluation, and distribution data. Passport data are a set of primary information for each accession, and accessible to the germplasm users (Fig.4). Also, an annual inventory of new accessions is released so that the users can know about the new acquisitions. Stock database is available on institute's intranet system for genebank management purposes. Characterization data, based on RDA crop-specific descriptors including image database are computerized for management and utilization of plant germplasm. A special software for taking image data of stored accessions was developed. This program helps to determine grain shape and measures their sizes. Image database also has a search function that can be used to identify unfamiliar specimens and accessions by matching the grain shape. The seed image database has been developed for the 25,000 conserved accessions of about 100 species. The information system of RDAGB can be accessed at *http://genebank.rda.go.kr/*. The database for vegetatively propagated PGR is under construction in collaboration with the institutions holding accessions in their field genebanks.

A new trial has been conducted to develop an integrated system for utilizing information of conserved germplasm. The integrated information system includes passport data, characterization data, GIS information, web-based core-set development, DNA profile data and their compounding data (Park *et al*. 2004). This system is more focusing on the utilization of PGRs (Fig. 4). The RDAGB is able to provide a processed data of each crop in case study for increasing utilization of stored germplasm.



<Main homepage of the RDAGB> <Integrated system for utilization>

Fig. 4. The main homepage for the RDAGB and a new integrated system of PGRS under the developing for providing characterization, core-sets, GIS ,and DNA profile data.

Policy and legislation

"RDA Genebank realizes its international obligations for sharing benefits arising from the use of introduced PGR and abides by the policies established under the auspices of the Convention on Biological Diversity (CBD) and the International Treaty of the FAO." The RDAGB believes in free-distribution of the germplasm it holds under international convention and with mutual agreement. The national management guideline of genetic resources for supporting germplasm activities was established under the Ministry of Agriculture and Forestry in 2007. The consideration for becoming a member of the ITPGRFA is subjected to relevant bodies under the government.

Future plan for PGR activities

The national program on plant genetic resources includes all the activities of public organizations such as government institutes and universities, and public sectors. There were more efforts for improving the national systems on sustainable conservation and utilization during last three years. The following descriptions are ongoing activities, which are strongly supported by the national program of plant genetic resources in Republic of Korea.

In situ conservation and development

a. Surveying genetic diversity of collections of *Camellia* species in Republic of Korea within the next two years.
b. Surveying Abies koreana at national level over the next three years.
c. Supporting on-farm management to restore diversity of landraces on farmers' lands.
d. Developing molecular systematics using molecular methods and evolutionary studies of genome diversification.

Ex situ conservation

a. Collecting and conserving wild *Pyrus* and *Malus* species from their natural habitat.
b. Collecting and conservation of landraces of persimmon from farmers' fields.
c. Developing national secure conservation system for genetic stocks and mutant lines for functional genomic research through cooperative project with research institutions and universities within the next 10 years.
d. Regenerating the accessions of low viability in collaboration with breeding institutions, organized by RDA (2009~2013).
e. Expanding the vegetatively propagated collections to university and private sector, in addition to the collections under RDA (2010~2012).
f. Developing in vitro and cryopreservation technology for lily, chrysanthemum and fruit trees within the next three years.

Utilization of plant genetic resources

a. Characterizing and evaluating 10,000 accessions through the cooperative projects with the breeding institutions.

b. Developing landrace core collection of barley, red pepper, Chinese cabbage and corn based on agronomic characters and molecular markers within the next three years.
c. Developing DNA profiles of core sets of main crops including UUC crops and vegetatively propagating crops, and molecular characterization methods to add value to PGR.
d. Constructing expression profiles of resistant genes in rice germplasm using RNA profiles.
e. Providing landrace varieties to farmers for assisting the development of sustainable agriculture systems.
f. Surveying under-utilized crop species according to their regional distributions and identifying their strong points in markets.
g. Developing and providing characterization and evaluation data for landraces of rice, soybean, barley and wheat to facilitate their uses in breeding programs.

Institutions and capacity building

a. Developing a strong national program for conservation and sustainable utilization of PGR in the Rep. of Korea, with a focus on PGRFA.
b. Developing a clearing-house mechanism to promote utilization of PGR originating from the Rep. of Korea including landraces and crop wild relatives.
c. Developing a safety backup system for duplication of plant genetic resources in Asian region through international cooperation.
d. Developing a web-based network program to provide characterization and evaluation data of PGR.

For implementing *in situ* conservation, the survey on wild relatives of crop species and on-farm collections will be continued on *Comellia, Pyrus* and *Diospyros kaki* for next several years. As for *ex situ* conservation, the RDAGB is establishing a national system for vegetatively propagating accessions which are independently maintained in each public institutes under the RDA. The seed collections in the universities are merging into one national conservation systems by national project now. The RDAGB has developed a managing system for networking of national collections of plant genetic resources.

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Status of Management of Plant and Animal Genetic Resources in Papua New Guinea

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Abstract

PNG has a diverse and rich resource base of plant, livestock and aquaculture genetic resources used for food and agriculture. These resources support livelihoods of the majority of rural population in the country. The safeguarding, maintenance and sustainable use of this genetic diversity is esential for current as well as future livelihood security. The National Agricultural Research Institute (NARI), as per its national manadate, maintains *ex situ* field gene banks as well as *in vitro* storages of major food crops including sweet potato, taro, banana, yam, cassava, taro, sweet potato and Aibika. Some indigenous and introduced fruit and nut crops are also maintained in *ex situ* collections, as are a small collection of both indigenous and introduced spices. NARI also maintains small conservation breeding stocks of sheep, goats, chicken, rabbits and ducks. The sustained use and development of these resources require supportive legislation and policy frameworks, which are still under development. Nevertheless PNG continues to collaborate with regional and international partners in the use and sharing of some of these resources. Currently the key constraints to sustainable utilization of these resources are lack of baseline information about the diversity and status of the resources, limitations in technical and logistical capacity in the design and implementation of appropriate management plans, lack of essential legal frameworks for use, access and transfer of these resources and the preceived continued threats on existing indigenous plant, livestock and aquatic resources from unsustainable utilization, large scale deforestation and expansion of human settlements.

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Introduction

The largely intact and prestine natural forests of Papua New Guinea (PNG), which cover up to 60% of the land mass (of about 462, 860 sq. km) provide natural habitat for a range of indigenous agricultural and forest genetic resources and their wild relatives. The country is also known to have one of the most heterogenous indigenous cultures and traditions with several thousands of separate communities maintaining their own language, customs and traditions for centuries in dense forests, valleys and islands. It is endowed with 3.12 million square kilometers of ocean area, together with 17,000 km of coastline, 4,250 km^2 deltaic plain /lagoon system and 4,180 km coastline around islands and atolls, inhabited by a wide diversity of marine and coastal flora and fauna, with huge potential for sustainable utilization. It also has numerous fast and slow flowing rivers and over 5,000 lakes with an extensive system of marshes located on the north and south parts of the country.

PNG is recognized as a major centre of genetic diversity for some traditional staple root/tuber crops, banana, leafy vegetables, fruits, nuts, and under-utilized crops species and forest trees (Kambuou, 1996). At least three quarters of the rural population in the country secures its livelihoods from the range of local plant, animal and fisheries resources, and hence the genetic diversities in these resources are of direct relevance to food security and livelihoods to the majority of the population.

Currently the National Agricultural Research Institute (NARI) of PNG is the custodian of the country's plant and animal genetic resources, having inherited initial activities and available infrastructure from the Department of Agriculture & Livestock (DAL) in 1996 (NARI, 2006a). NARI now maintains several *ex situ* field gene-banks of the major staple food crop species and two small tissue culture facilities. It also maintains breeding stock of introduced breeds of some livestock species (sheep, goats, rabbits, ducks, chicken). A few commodity-based institutions also maintain germplasm collections of industrial crops, such as coffee, cocoa, coconut and sugarcane (Kambuou, 1996; 2007).

This report reviews the current state of knowledge on the identification, maintenance and utilization of plant, livestock and aquatic genetic resources of PNG and brings out known constraints in the sustainable utilizaton of these resources.

Plant genetic resources for food and agriculture

Kambuou (1996) has provide an extensive review of the known diversity of plant genetic resources in PNG, particularly for the traditional root and tuber crops, bananas and green leafy vegetables, for which PNG is known to be a secondary centre of diversity.

Sweet potato (*Ipomoea batatas* L. Lam) is the main root crop in PNG in terms of production and consumption. It is widely cultuvated from sea level to 2700m with main production in the highlands. Over the years over a thousand accessions of sweet potatoes were collected and assembled in *ex situ* establishments in the country (Kambuou, 1996; 2007); these are mostly landraces, farmers' cultivars and common varieties.

The second most important root crop is taro (*Colocasia esculenta* L. Schott), and is considered as one of the indigenous traditional food crops of PNG. Although it is predominantly grown in the low altitude rainforest areas, it is being grown in highlands of up to 2700m altitude. Over 763 indigenous accessions of mostly landraces and farmers' cultivars were collected and assembled in *ex situ* collections in the country (Kambuou, 1996; 2007).

The yams (*Dioscorea* spp.) are the third most important root crop of the country, and up to 400 accessions of yams were collected and asembled in *ex situ* collections. Cassava is not native to PNG but is the main staple crop in coastal areas. Up to 115 accessions, mostly landraces and farmers' cultuvars, have been collected and assembled in *ex situ* collections.

Over 40 species of edible green leaf vegetables in PNG had been collected. The most popular species include Aibika (*Abelmoscuhus manihot* L. Medik), *Amaranthus* spp., Tulip (*Gnetum gnemon* L.), Rugia (*Rugia klossil* S. Moore), water dropwort (*Oenanthe javanica* D.C.), Blackberried nightshade (*Solanum nigrum* L.), Kumu mosong (*Ficus* spp.), Kangkong (*Ipomoea aquatica* Forskal), Watercress (*Nasturium spp*.) Valangular (*Polyscias spp*.), Kumu grass (*Callipteris prolifera* Lam. Bory), Choko tips (*Sechium edule* Jacquin Swartz) and Pumpkin tips (*Cucurbita moschata* Duch et Lam), all of which are either cultivated in the gardens or grown in the wild. Some of these species have great intra-specific variations. For example, over 140 Aibika accessions of landraces and farmers' cultivars had been collected from all over the country (Kambuou, 1996; 2007).

PNG is an important centre of distribution of wild banana, and has the greatest genetic diversity of botanically primitive diploid cultigens amongst large numbers of cultivars. Bananas are grown all over the country and they are important staple food crops in the

coasal low altitide areas. According to Argent (1976; cf. Kambuou, 1996), two genera of family Muaceae are found in PNG - genus Ensete, represented by one species, *Ensete glaucum,* and genus Musa, represented by nine species. Kambuou (1996) reported that some 800 accessions of both cultivated and wild bananas from PNG were collected and assembled; but only about a quarter of this number are in national field collections. Fruit species native to PNG include wild mangoes (*Mangifera* spp.), bukbuk (*Burckella obovata* Forst Pierre), a native fruit of the Atolls of PNG, Marita (*Pandanus conoideus* Lamarck), taun (*Pometia pinnata*), golden plum (*Spondias cytherea* Sonnerat), the tree cucumber or Bilimbi (*Averrhoa bilimbi* L.) and a number of introduced citrus species.

Coconut is a widely occuring and cultivated nut species consumed throughout the country. It is also an imprtant cash crop. The same is true about Betel nut (*Areca* spp). Six *Pandanus* species, four edible *Canarium* species (also known as Galip nut), and five edible *Terminalia* species (Okari) are reported in the country. Another popular nut tree species is Pao (*Barringtonia novae herbernae* Laut). Others are the PNG oak or Castanopis chestnut, the finschia nut, the tahitian chestnut, the candle nut (*Aleurites moluccana* L. Wild), the Nipa palm (*Nipa fruticans* Wurmn) and Pangi (*Pangium edule* Reinw), also locally known as Sis (Kambuou, 1996).

Unlike the Asian neighbours people in PNG use very little spice in their food, and almost all spices commonly used in their food are introduced species. Only a few indigenous species are used as herbs or flavourings in some local dishes. Some of these are the ginger, the Begonia (*Begonia* spp), *Coix gigantea* Koenig et Roxb, *Coleus scutellarioides*, *Euodis* spp and the Fennel plant (*Foeniculum vulgare* Mill).

PNG is the centre of origin of the ‘Noble cane’ (*Saccharum officinarum*). There is also substantial diversity of this species being cultivated in subsistent gardens in a wide range of environments from the coast to the highland areas; more notably it cannot survive in the wild. Kambuou (1996) reported that a total of 206 accessions were collected during the 1977 expedition, but little was documented about the composition of this collection.

Reported research work on pasture and forages focused on introduced species; the native pasture species of PNG are yet to be identified or recorded. In 1980 some 500 accessions of Desmodium species were collected by CSIRO researchers and transferred to Australia without duplicate collections being maintained in PNG. There is no current work on indigenous pasture and forage species.

Management of plant genetic resources

Through financial and technical assistance from the former International Plant Genetic Resources Institute (IPGRI) and bilateral regional support, PNG has undertaken series of projects for the collection of germplasm in traditional food crops throughout the country and established *ex situ* gene banks at research stations of initially the Department of Agriculture and Livestock (DAL), and since 1996 the NARI. The NARI has subsequently developed a genetic resources program to coordinate management of genetic resources at national level (NARI, 2006 a,b). The national plant genetic resource (PGR) collections for the traditional food crops are currently being held at Laloki, Aiyura and Kerevat research stations representing the three major agroecological zones of the country – the dry lowlands, the mainland highlands and the low lying wet islands regions, respectively. Working collections of these germplasm are also maintained at these and other research stations of NARI. It is expected that these collections are regularly replanted to regenerate new and healthy materials and are also checked for mixtures to avoid contamination of materials in the field (NARI, 2006b), but these have not been consistently implemented as noted from reports of losses and admixtures. The current national collections include 1209 accessions of sweet potato, 763 accessions of taro, 221 accessions of banana, 234 accessions of yam, 95 accessions of cassava and 49 accessions of Aibika (Table 1). In addition, a range of fruit, nut and spice species and varieties, including the rambutan, mangosteen, durian, guava, taun, galip nut, nutmeg, pepper and kava are maintained in field gene banks.

While these are maintained as *ex situ* collections, most of the landraces and farmer cultivars are assumed to continue to survive under *in situ* conditions with farmers or exist in the wild along with their wild progenitors, but this will need to be verified. For instance, out of over 300 accessions of taro identified in the early 1980s in the coastal Huon Gulf district of Morobe Province, only a limited number of more marketable common cultivars are maintained by many farmers at the expense of the wide range of taros that they once maintained (Kambuou, 1996). Similarly Apa (2006) reported that a 2005 survey of Gabadi-Mekeo area of Central Province revealed that farmers maintained only eight of the 15 common banana cultivars recorded some nine years earlier.

Table 1: The numbers of accessions currently held in national core and working collections by NARI (Kambuou, 2007)

Crop	Scientific name	National	Working	
		(Field)	Field	Tissue
Sweet potato	*Ipomea batatas*	1209	80	72
Banana	*Musa spp*	221	107	23
Taro	*Colocasia esculenta*	763	101	5
Yam	*Dioscorea spp*	234	9	
Cassava	*Manihot esculenta*	95	87	
Aibika	*Abelmoschus manihot*	49	60	
Irish potato	*Solanum tuberosum*		41	59
Chinese Taro	*Xanthosoma sigatifolium*		3	
Swamp taro	*Cyrtosperma chamissionis*		2	
Andean tubers			3	
Various traditional vegetables			22	

Even among the registered collections, a good number of accessions of the major crops have been reported as lost due to technical and logistical constraints. An economic assessment of the costs and benefits of field germplasm maintenance activities of major food crops conducted in 2001 (Wells and Eldridge, 2001) not only established the case for continued resource allocations on this activity at national level, but also affirmed the need for regional collaboration in germplasm management both to facilitate sharing of resources and reduce maintenance costs for germplasm collections.

In terms of *in situ* conservation, three officially recognized national parks with a number of nature reserves in them are being maintained. These are owned by land owners and government employed park rangers maintain them on site, and ensure that these areas are kept free of any agricultural or logging activities (Kambuou, 1996).

Livestock genetic resources

A comprehensive survey or census of livestock genetic resources of PNG is yet to be undertaken. Only crude estimates of livestock populations were made in 1982, 1993 and in 2002 (Table 2).

Table 2. Important livestock species, known breeds and their population estimates

Species	Breeds	Important features	Population estimates (Quartermain, 2002)
Pigs	Native	Tolerance to fibrous feeds, internal parasites	1.8 million in 2002
	Large White, Landrace, Saddle Back, Duroc, Tamworth	Variable attributes	32,000, all in commercial herds
Chicken	Native chicken	Scavenging, broody, tolerant to parasites, with high mortality losses and low production	1.5 million
	Australorps	Dual purpose meat and egg type, adaptable to scavenging	Onle several hundred known purebred populations currently maintained by NARI and OKTedi.
	Ross strain broilers	Commercial inbred broilers	Parent stocks maintained by commercial companies
	Shaver Brown	Commercial inbred layers	Parent stocks maintained by a commercial company (Zenag)
Cattle	Javanese Zebu	Hardy; tolerant to tick and screw work infestation; adapted to poor pasture; have short calving interval; found only in the Sepik plains	400~600; perhaps decreasing in size; down from an estimate of 2000 in 1982. Breed status may be endangered.
	Brahman, Droughtmaster, Santa Gertrudis, Aberdeen Angus, Hereford	Comemrcial beef breeds	In large and small commercial herds; no reliable population estimates available
	Friesian Jersey	Commercial dairy breeds	In large and small commercial herds; no reliable population estimates available
Sheep	Highlands Halfbred		About 15,000 and increasing
	Priangan	High incidence of multiple births	
Goats	Mixed breed	High incidence of multiple births	20, 000~25, 000
Ducks	Muscovy	Dual purpose and versatile	10,000 flocks
	White Campbell, Khaki Campbell, Indian Runner Rouen	Mainly egg type, hardy	3000
Rabbits	New Zealand White	Suited to highlands	20,000
	Canberra Halflop	Suited to lowlands	
Swamp buffalo		Mainly found in the Sepik plains as feral populations; but also in Madang, Morobe and East New Britain Provinces as draught animals.	4000

In PNG, indigenous pigs appear to be the most important livestock species to smallholder livestock keepers, be it in terms of population size and distribution, contribution to livelihoods or socio-cultural significance. They also have a much longer evolutionary history than other livestock species. But their genetic diversity is largely unknown. With several hundred different ethnic groups and languages and numerous isolated traditional communities that exist in the country, the pig genetic diversity may have particular relevance for detailed genetic studies (Ayalew, 2007).

The indigenous chicken populations in the mainland as well as major islands appear to have been subjected to extensive genetic admixture from introduced improver breeds such as Australorps which have been promoted indiscreminately over the last several decades. However, as the Australorp chicken are not broody, replacement of pure breeding stock has always been a problem to smallholder farmers. Thus the Australorp chicken of smallholder farmers were either not sustainably maintained in pure stock in the villages, or are often kept together with village chicken, leading inevitably to continual uncontrolled crossing and interbreeding. Detailed genetic studies are needed not only to quantify the existing genetic diversity in the native village populations but also to gauge the level of genetic introgressions from introduced genotypes (Ayalew, 2007). On the other hand, the commercial broiler and egg industries which use commercial inbred lines of exotic genotypes, are very strong in PNG, engaging up to 55 thousand smallholder farmers in a grow-out model for contractual broiler production (Glatz, 2007).

The existing sheep and goat populations in PNG evolved from interbreeding of exotic breeds introduced into the country mainly during the colonial and post-colonial period in the past 100 or so years (Quartermain, 2002). No indigenous populations are known to exist in the country. The Priangan and Highland halfbred that exist today must have evolved as composites of these breeds at various proportions. It is therefore hypothesized that the existing sheep populations have a narrow genetic base. Similarly, the existing goat populations are believed to have evolved from remnants of a variety of dairy-type goats introduced during the early colonial period (Quartermain, 2002). More recently some feral goat populations from Australia and New Zealand were introduced to genetically reinforce the village goat flocks. Mainly goats but also sheep are becoming increasingly popular livestock species for smallholder farmers in the high and mid altitude areas of the country (Ayalew, 2007).

There is no native cattle breed in the country; the Javanese zebu was introduced from Indonesia and Australia, and their numbers are very low and hence recognized as endangered. The surviving population is presumed restricted in the Sepic plains in the northern mainland of the country, some of them reportedly surviving as feral herds. Several other exotic commercial beef breeds introduced from Australia are mainly kept by commercial ranches (MoA&L, 2004).

Management of genetic resources

PNG has a national coordinator for farm animal genetic resources appointed from the Ministry of Agriculture and Livestock to coordinate core activities. However, the coordination activity has been rather weak, and researchers from other institutions (NARI, Unitech and NAQIA) have taken up such activities as the preparation of the Country Report to the State of the World's Animal Genetic Resources for Food and Agriculture (MoA&L, 2004) and networking. The national farm animal management strategy proposed in the Country Report did not proceed to implementation stage. Generally the development and sustainable utilization of farm animal genetic resources have not been a priority development activity in PNG. One possible reason is lack of qualified manpower in this area.

As per its national mandate, NARI currently maintains *ex situ* conservation flocks in its research stations mainly as a source of selected breeding animals to supply smallholder farmers. These include some 250 breeding ewes of Highland Halfbred sheep at Tambul, 30 breeding ewe of Priangan sheep at Labu; 70 breeding does of goats; 50 rabbit does; 50 Australorp laying hens; 30 native village chicken, 70 breeding Muscovy ducks and 70 layer true ducks. The goat, Australorp and rabbit flocks are currently maintained in duplicate *ex situ* conservation breeding flocks. A growing number of smallholder farmers are raising goats, sheep, Muscovy ducks and rabbits; however, except occasional exchanges and sales of breeding stock, these flocks do not have formalised functional relationships with the breeding flocks maintained in the research stations to manage risks of loss of genetic diversity. The conservation flocks are therefore vulnerabe to natural and man-made disasters that can lead to sudden loss of whole breeding flocks. For livestock genetic resource, the most effective strategy to conservation is to sustainably utilize the resources in their natural habitat by encouraging and supporting the traditional livestock keepers.

There are no facilities for the collection and storage of cryopreserved genetic material (semen, ova, embryos) for purposes of genetic improvement or conservation. Facilities to carry out molecular studies are not available in the country.

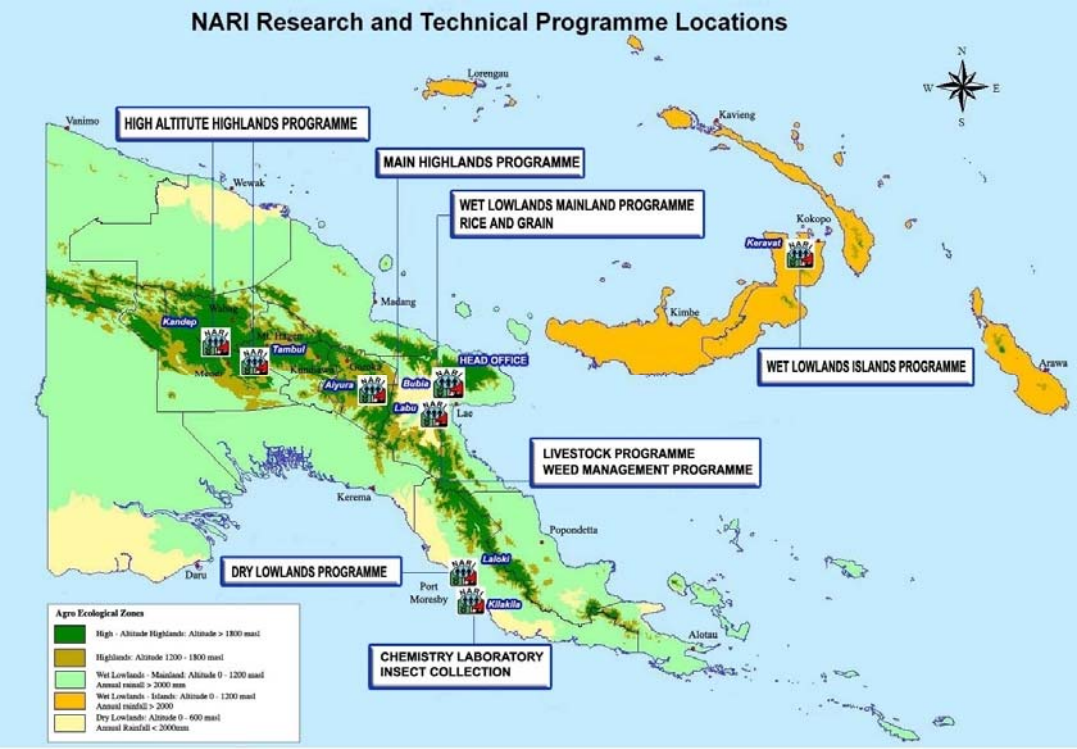

Figure 1. Political map of Papua New Guinea showing the location of research stations of NARI involved in *ex situ* maintenace of germplasm collections

Aquatic genetic resources

As stated above, PNG has an extensive resource base for marine fisheries. The abundant rainfall and fertile soils also make inland aquaculture a viable option for rural communities in most parts of the country. Located in the tropics, PNG is home to most of the important tropical aquaculture species: barramundi (*Lates calcarifier*), freshwater prawns (*Macrobrachium rosenberghii* and other *Macrobrachium* spp), freshwater crayfish (*Cherax albertsii*), tropical seaweeds, sea cucumber (*Holothuria* spp), tropical sponges and corals, groupers, marine prawns (*Penaeus* spp), mud crabs (*Scylla* spp), giant clam and pearl oysters (FAO, 2002; Smith *et al.,* 2007). It also has a great diversity of freshwater and marine

environment for aquaculture. There is a tremendous potential in inland aquaculture given that captured fisheries has become increasingly commercially unsustainable.

Unlike developments in other island countries in Asia, aquaculture in PNG is a recent activity as compared to agriculture and animal husbandry, but with well coordinated awareness and training, it can play an important role in improving food security and contribute to sustainable rural development (NFA, 2004).

In an effort to increase local fish stocks, numerous exotic fish species were introduced into PNG. The introductions of fish species before 1990 were either illegal or planned without proper quarantine procedures, but after 1990, import protocols were established and enforced (Coates, 1989; Kolkolo, 1996). In total, about 200 fish species have been introduced to PNG in an attempt to improve wild fish and aquaculture production, recreational fishery and aquarium (Smith *et al,.* 2007). Based on preliminary indications, it is hypothesized that some introduced species have led to undesirable changes in the composition of native fish stocks in some water bodies.

Relevant national legislation

A draft bill on access and benefit as well as modalities for material transfer agreements on genetic resources is currently under discussion and it is hoped that the bill will be enacted very soon. PNG has strong quarantine protocols for import of any germplasm and materials that are deems risky for the maintenance of native genetic resources in the country. Currently, there are no formal national legal frameworks for transfer of plant, animal or aquatic genetic resources out of PNG; informal arrangements between concerned international parties are being used to transfer genetic materials even for research purposes. It is recognized that genetic materials transfererd without a proper MTA prorocol are not safeguarded from unauthorized commercial uses.

PNG has an operational national aquaculture policy that identifies the major constraints to fisheries and aquaculture development in the country as well as the strategies for nation-wide development of aquaculture (NFA, 2004). But the policy does not cover the management of native fisheries genetic resources of the country. Facilities for quarantine and conservation of fisheries genetic resources are yet to be established.

PNG does not have any direct or indirect public incentive to farmers for their continued maintenance and conservation of indigenous crop, livestock or fisheries genetic resources.

Collaboration and networking

PNG is taking active part in various regional and international collaborative projects and networks related to the management of germplasm, including the Pacific Agriculture Plant Genetic Resources Network (PAPGREN). It also collaborates with the Centre for Pacific Tree and Crops (CePaCT), the Banana-Asia Pacific Network (BAPNET) and the Bioversity International in the sharing and maintenace of plant genetic resources. National networks relevant to the management of germplasm are the Papua New Guinea Biodiversity Network (PNGBioNET), the National Biotechnology & Biosafety Network and the National Biodiversity Strategy and Action Plan (NBSAP) under the Department of Environment & Conservation (DEC).

PNG is also taking part in regional initiatives for the characterization and documentation of existing farm animal genetic resources of the South Pacific Region. The South Pacific Community, to which PNG is also a member, provides technical and financial support as part of regional initiatives in the management of genetic resources.

Major constraints in the management of GR

1. Incomplete, or lack of, baseline information on the identity, diversity, distribution, utilization and current status of plant, animal and aquatic genetic resources. At least all the *ex situ* collections need to be fully characterized and documented in the form that can be easily accesible nationally and internationally.
2. Limited technical and logistic capacity in the design and operationalization of appropriate programs for the management of genetic resources, that encompass and, as appropriate, combine complementary *in situ* as well as *ex situ* modes of conservation. Numerous accessions from collections have been lost over time due to limitaions of maintaining *ex situ* collections; others have been identified later as duplicates. Uncontrolled contaminations have also been reported.
3. Lack of necessary national ABS and MTA protocols to formalize transfer of genetic materials across borders.
4. Absence of national management plans for at least the major plant, animal and aquatic genetic resources with direct relevance to food and agriculture. Contingency plans are yet to be developed to avert disasterous losses of genetic resources in the event of

major natural and man-made catastrophes. For instance, a whole collection of 423 yam accessions were lost from the Laloki research station in 1995 when budgetary allocations were cut back and no replanting was done subsequently.

5. Perceived continued threats to the maintenance of genetic resources from large scale deforestation due to logging, expansion of human settlements into hitherto uninhabited natural forests and unsustainable utilization of native plant, animal and aquaculture getetic resources.

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Management of Biodiversity and Conservation of Genetic Resources for Food and Agriculture in Peru

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Abstract

Peru has high ecological diversity, diverse climates, extensive ecological zones, large production areas, and highly productive ecosystems, which have supported high biodiversity, leading it to be recognized as a mega-diverse country and one of the world's most important centers for plant and animal genetic resources. Also associated with this biodiversity is high cultural diversity.

Laws of international, regional, and national scope have been ratified and/or enacted in Peru, for the purpose of promoting conservation, sustainable use, and access to genetic resources under an ecosystem approach. In addition, laws have been enacted to protect the collective knowledge of indigenous people linked to biological resources, and also to ensure that the use of biotechnology does not harm biodiversity or the environment.

The National System of Protected Natural Areas of the Peruvian State is the main *in situ* conservation system of biological diversity; currently it includes 63 protected areas which represent 14.80% of the total area of the country. In addition, there are many plant and animal germplasm banks in which 54,351 accessions are conserved *ex situ* under medium- to long-term storage conditions.

In situ conservation of plant genetic resources has been practiced since ancestral times by local farmers, especially in the Andean region. Since the beginning of the 1990s, many projects of *in situ* conservation have been executed in different regions of the coast, mountains, and jungle, with the objective of studying the dynamics of this type of conservation, establish biodiversity microgenecenters, conduct seed fairs, and develop records of

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traditional varieties and their wild relatives and of conservationist farmers' practices. Peasant communities, together with non-governmental organizations (NGOs) and regional governments, are promoting the recognition of geographical areas so that the resources there can be properly managed, including the components of biodiversity and genetic resources.

The Subdirection of Genetic Resources and Biotechnology of the National Institute of Agricultural Innovation has developed an information system (currently in the test phase) for managing information of its germplasm bank, and it also has been considered for inclusion in implementing the GRIN GLOBAL information system of genetic resources.

A complete system for managing genetic resources for food and agriculture must include the conservation of genetic resources (both *ex situ* and *in situ* conservation), the development of infrastructure for conservation, especially for the long term, and the development of human capabilities and information systems.

Peruvian biodiversity

Peru is located in the central and occidental part of South America, with a continental extension of 1,285,216 km^2, with 136,233km² (10.6%) in the coastal region, 404,843 km² (31.5%) in the Andean region, and 754,140 km² (57.9%) in the Amazonian region. It encompasses 25 political regions.

It has high ecological diversity, diverse climates, varied ecological zones, large production areas, and highly productive ecosystems[2]. All these have supported elevated biological diversity (biodiversity), and Peru is recognized as a mega-diverse country. In addition, it is the center of origin of many important crops and breeds, and also wild relatives of domesticated species. In consequence, it is one of the world’s most important centers for plant and animal genetic resources. This biodiversity has also spurred high cultural diversity, expressed in 70 ethno-linguistic groups with large experience in conservation and sustainable use of genetic resources, especially crops and plants for medicinal uses in the Amazonian and Andean regions.

There are 128 species of native plants domesticated with hundreds or even thousands of varieties, and also wild forms of these plants. For instance, there are nine domesticated species of potato with 4000 varieties and 85 wild species; and there are 15 species of tomatoes. In terms of fauna, there are five domesticated animals: the alpaca, a domesticated

[2] Brack E., A. 2000. Peru a wonderful country.

form of the vicugna (*Lama vicugna*); the llama, a domesticated form of the guanaco (*Lama guanicoe*); the guinea pig, a domesticated form of the poronccoy (*Cavia tschudii*); the criollo duck, a domesticated form of the Amazonian duck (*Cairina moschata*); and the suckling pig (*Dactilopius costae*) associated with the prickly pear crop.

It is estimated that approximately 65% of national agriculture depends on native genetic resources, among which are grains (quinua, *Chenopodium quinoa*, kiwicha, *Amarantus caudatus,* and cañiwa, *Chenopodium pallidicaule*) of great potential as a future source of food for humanity because of their high protein value; fruits; roots (yacón, *Smallanthus sonchifolia,* arracacha, *Arracacia xanthorriza,* and maca, *Lepidium meyenii),* Andean tubers, and legumes. An important part of the national livestock production depends on native genetic resources, especially camelids.

Instruments for biodiversity management

The Peruvian Political Constitution[3] declares that natural resources, renewable and non-renewable, are part of the national patrimony, the state promotes their sustainable use, and it is obligated to promote biodiversity conservation and protect natural areas[4].

The planning and management of biodiversity that includes genetic resources is regulated by the Convention on Biological Diversity (CDB)[5], the Regional Strategy for the Biodiversity for Tropical Andean Countries (ERBD)[6], the *Law of Conservation and Sustainable Use of the Biological Diversity*[7] and its regulations[8], and the National Strategy on Biological Diversity (ENDB)[9]. These are complemented by the *Law for Management and Sustainable Use of Medicinal Plants*[10], the *Mark Law for the National System of Environment*

[3] Ratified by Referendum October 31st, 1993.
[4] Articles 66, 67, and 68 of the Political Constitution of Peru.
[5] Approved in the Rio Summit in June 1992, ratified by Peru through a Legislative Resolution No. 26181.
[6] Decision No. 523, Lima - Peru, July 7th, 2002.
[7] Law No. 26839, January 17th, 1997. Its objectives are regulating the conservation of biological diversity and sustainable use of its components, and incorporate the principles and definitions of the CDB.
[8] Supreme Decree No. 068-2001-PCM, Publisher on July 21st, 2001 at the official newspaper El Peruano.
[9] Supreme Decree No. 102-2001-PCM, September 4th, 2001.
[10] Law No. 27300, promulgated on June 15th, 2000.

Management[11] and its regulations[12], the *General Law of the Environment*[13], and the *Law for the National Protected Areas*[14].

These instruments at the international, regional, and national levels recognize the sovereign rights of states over their natural resources and also the importance of their conservation and sustainable use. In Peru, they also define a ecosystem approach for managing biodiversity, prioritizing conservation aspects (ecosystems, species, and *in situ* and *ex situ* genetic resources), integrating sustainable use (genetic resources access, biosafety, etc), providing special measurements for conservation and restoration of biodiversity (control of invasive species, modified living organisms, etc), committing and participating in Peruvian society, and also promoting the investigation, assessment, protection, and strengthening of knowledge, innovations, traditional practices, and capacity building.

The Natural Protected Areas (ANP) are continental or marine areas of the national territory, dedicated to biodiversity conservation and other scientific-, cultural-, and scenic-related values; they constitute the national patrimony and are kept for perpetuity. Under state administration, they constitute the National System for the Natural Protected Areas (SINANPE), and are also under regional or local government administration and also private administration. Carrying out SINANPE management is delegated to the National Institute of Natural Resources (INRENA).

The National Program of Agro-Biodiversity[15] that prioritizes the conservation and sustainable use and participative management of agro-biodiversity, beginning from the identification, characterization, and valuation, and respect for local cultures, is actually in the process of being implemented by regional governments. The Technical Secretary of the Program is in charge of the Biodiversity and Biosafety Unit of the Environment Ministry (MINAM)[16] (formerly the National Environment Council).

In addition, the MINAM is now promoting the establishment of *ex situ* conservation centers of the Biological Diversity Network, that includes germplasm banks and conserved species for food and agriculture; and also possession and management centers that are

[11] Law No. 28245, promulgated on June 4th, 2004.
[12] Supreme No. 008-2005-PCM, promulgated January 28th, 2005.
[13] Law No. 28611, promulgated October 13th, 2005.
[14] Law No. 26834, promulgated June 17th, 1997.
[15] Decree of the Directive Council No. 022-2004-CONAM/CD, November 26th, 2004.
[16] Resolution of the Executive Secretary No. 004-2005-CONAM/SE, November 12th, 2005.

comprised of faunal centers (zoos, rescue centers, transit centers, zoo breeding centers, and museums) and floral centers (botanic gardens, nurseries, and herbariums).

Access to genetic resources

Access to genetic resources contained in biodiversity and derived products is regulated by the CBD, the International treaty for Plant Genetic Resources for Food and Agriculture of the United Nations Organization for Food and Agriculture (TIRFAA)[17], the common regimen of Common Access of the Genetic Resources[18], the *Forestry and Wild Fauna Law*[19] and its regulations[20], the Genetic Material Transfer Agreement that some *ex situ* conservation centers possess (International Potato Centre; CIP), and the National Institute of Agrarian Innovation (INIA)[21]. The INRENA also has developed some formats of Genetic Material Transfer Agreements for wild species and microorganisms, especially for scientific research.

These regulations define the sovereignty of countries over their genetic resources and derived products, and in consequence determine their access conditions. Access to genetic resources and activities of bioprospecting of biodiversity that involve wild floral and faunal species at *in situ* conditions are regulated by the *Forestry and Wild Fauna Law* and its regulations, and INRENA is the institution in charge until the regulation of the Common Regimen of Access to Genetic Resources is approved.

The regulation proposal[22] that stipulates that the Common Regimen of Access to Genetic Resources be effectively implemented is now at MINAM for promulgation. MINAM is in charge of the inter-sectorial coordination for environmental affairs including biological resources that encompass genetic resources, and the National Commission for Biological Diversity (CONADIB) is the multisectorial consultative agency responsible for policies on the conservation and sustainable use of biological resources.

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[17] Approved by Supreme Decree No. 012-2003-PCM, published at the official newspaper El Peruano, January 27th, 2003.

[18] Decision No. 391, Adopted in Caracas on July 2nd, 1996, based on the third transitory disposition of Decision 345 of the Commission and the proposal 284/rev.1 of the board, was published by the official gazette on July 17th, 1996.

[19] Law No. 27308, July 15th, 2000. The law defines that the forestal resources comprehend wild species of emerging terrestrial and aquatic flora as biological resources that contain genetic resources or their derivates.

[20] Supreme Decree No. 014-2001-AG, published by the official newspaper El Peruano on April 9th, 2001.

[21] Jefatural Resolution No. 117-2001-INIA, July 2nd, 2001

[22] Second proposal of Decision No. 391 Regulation, prepared by the National Commission of Biological Diversity-CONADIB.

The competent authorities in charge of the evaluation of the appropriateness of the applications and access projects are INRENA for genetic resources and natural molecules contained in continental wild species; INIA for genetic resources and molecules contained in cultivated and domestic continental species; and the Vice Ministry of Fisheries of the Production Ministry for genetic resources and molecules contained in continental and marine hydro-biological species.

Traditional knowledge protection

The regimen for the protection of the collective knowledge of indigenous people linked to biological resources[23] has established three types of registries: 1) confidential knowledge, 2) public domain knowledge, and 3) local registries (in charge of indigenous people), and the Direction of Inventions and New Technologies (DIN) from the National Institute of Competition Defence and Protection of Intellectual Property (INDECOPI) is the national competent authority. Nowadays, the National Public Registry (public domain knowledge) has more than 200 registries supported by at least one publication. Many indigenous communities are developing local registries.

Biosafety

Biotechnology and its rational management, especially the development of safe biotechnologies for biodiversity and the environment established in the 21st Agenda[24] and the CDB are regulated in Peru, and that is why our country has ratified the Protocol of Cartagen[25] on the safe use of biotechnology. At the Andean community (CAN) level, decisions such as the Common Regimen for Protection of the Breeder's Right of Plant Varieties[26], Common Regimen of Genetic Resource Access[27], and the ERBD contemplate the development of biotechnology and biosafety mechanisms.

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[23] Law No. 27811, published in the Official Newspaper El Peruano on August 10th, 2002.

[24] Program of United Nations (ONU) to promote the sustainable development of the community, in equilibrium with the natural capital and with the local economic capacities, approved at Rio de Janeiro Summit in June 1992.

[25] Legislative Resolution No. 28170, published at Official Newspaper El Peruano on February 15th, 2004.

[26] Decision No. 345, approved October 21st, 1993.

[27] Decision No. 391, approved July 2nd, 1996.

Thus, Peru has promulgated the *Law for Risk Prevention of Derived Uses of Biotechnology*[28] and its regulations[29], and is in the process of implementing Competent Sectorial Organisms. This ruling regulates different activities with modified living organisms (OVMs), at different stages from the research level, production, introduction to commercialization, and confined use, and liberation under controlled conditions. In addition, it defines the institutional design for a biosafety legal mark supported by three pillars: competent distribution among the sectorial organisms, conformation of a technical advisory committee, and their coordinated performance through an intersectorial organism, the MINAM.

The OSC includes the INIA, Fishery Vice-ministry of the Production Ministry, and the General Direction of Environmental Health (DIGESA) of the Health Ministry, for agriculture, fishery, and health sectors, respectively. INIA has incorporated this mandate in its Organization and Functioning Regulation (ROF)[30] and has created its Biosafety Intern Committee (CinBio)[31] and approved CinBio's ROF[32].

The legislative decree that regulates the Agrarian Innovation National System[33] granted INIA the authority to sanction, in the scope of its competence, typify, and qualify infractions included in the biosafety sectorial regulation proposal that is in the approval process.

Conservation of biodiversity

SINANPE is the most important system for the *in situ* conservation of biodiversity in Peru. Nowadays, it encompasses 63 natural protected areas that represent almost 14.8% of the total country surface, placing Peru among Latin American countries with a higher percentage of territories conserved under this modality (19,041,079 ha). SINANPE includes categories such as, national parks, national sanctuaries, historic sanctuaries, national reserves, wildlife refuges, landscape reserves, communal reserves, protected forests, game preserves, reserved zones, and also regional and private conservation areas.

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[28] Law No. 27104, promulgated on May 7th, 1999.
[29] Supreme Decree No. 108-2002-PCM, promulgated on October 21st, 2002.
[30] Supreme Decree No. 031-2005-AG, July 13th, 2005.
[31] Jefatural Resolution No. 00124-200/-INIA, May 08th, 2008.
[32] Jefatural Resolution No. 00232-2007-INIA, September 21st, 2007.
[33] Legislative Decree No. 1060, published at Official Newspaper El Peruano on June 28th, 2008.

Conservation of genetic resources for food and agriculture

Ex situ conservation

In Peru, germplasm banks of plant and animal genetic resources are mainly distributed among research institutes, universities, and NGOs. Gutierrez and Sigüeñas (2002) reported that 22 institutions have germplasm banks, of which 11 are public and 11 private. Among private institutions, five are from NGOs. They are preserving 54,351 accessions representing 255 species. Among these, 62.4% have passport data, 63.9% have morphological data, and 48.8% have agronomic data such as performance, tolerance to stress, and resistance to pests and/or diseases of the total accessions. They carry out short- and medium-term conservation, with the exception of the IPC, which conducts long-term preservation through cryopreservation.

The INIA through the SUDIRGEB is officially responsible for the conservation and sustainable use of genetic resources of agro-biodiversity and for enhancing its value, either as food security or as source of genetic resources for breeding programs. Conservation is carried out through a network of ten Agricultural Experimental Stations that mainly preserve genetic material from native crops.

The SUDIRGEB-INIA owns the largest germplasm bank of the country, comprising 30 national collections categorized as crops or crop groups, which preserve 17,147 accessions from 201 species in three forms: in the field, *in vitro*, and in cold rooms. The IPC maintains 16,958 accessions for crops such as potatoes, sweet potatoes, and other Andean roots and tubers, and the La Molina Agrarian National University (UNALM) preserve 3023 accessions of maize. In terms of the conservation of native species of medicinal plants, the Research Institute of the Peruvian Amazon (IIAP) reported owning a Botanical Garden of Medicinal Plants in its Biological Station Allpahuayo in Iquitos (Table 1).

In addition, a seed bank of forest species was reported, which is responsible to the National Project for Watershed Management and Soil Conservation (PRONAMACHCS).

Table 1. Institutions that have *ex situ* germplasm banks of plant genetic resources

Institution	Sector	Region	No. of accessions
National Institute of Agricultural Innovation (INIA)	Public		
Subdirection of Genetic Resources and Biotechnology (SUDIRGEB)			
– Headquarters		Lima	2166
– EEA Andenes		Cusco	3115
– EEA Baños del Inca		Cajamarca	2220
– EEA Canaán		Ayacucho	1912
– EEA Donoso		Lima	1566
– EEA El Porvenir		San Martín	338
– EEA Illpa		Puno	3738
– EEA Pucallpa		Ucayali	125
– EEA San Roque		Loreto	196
– EEA Santa Ana		Junín	1771
National Program of Research in Corn and Rice (PNIMA)			
– EEA Vista Florida		Lambayeque	196
– EEA El Porvenir		San Martín	2213
National Program of Research in Fruits (PNIF)			
– EEA Baños del Inca		Cajamarca	47
– EEA Santa Ana		Junín	40
– EEA Pucallpa		Ucayali	100
National Program of Research in Tropical Crops (PNICT)		San Martín	48
National Program of Research in Pasture and Forage (PNIPF**)**			
– EEA Baños del Inca		Cajamarca	20
– EEA El Porvenir		San Martín	125
National Program of Research in Andean Crops (PNICA)			
– EEA Canaán		Ayacucho	957
– EEA Santa Ana		Junín	1841
National Program of Research in Potato and Sweet Potato (PNIPC)			
– EEA Santa Ana		Junín	666

Research Institute of the Peruvian Amazon (IIAP)	Public		
– CRI-IIAP-San Martín		Tarapoto	18
– Promising Native Fruit Project, Medicinal Plants and Biocides		Iquitos	59
– Palmeras Project and Plant Genetic Resources			120
Universities			
Pedro Ruiz Gallo National University	Public	Lambayeque	64
Jose Faustino Sanchez Carrion National University	Public		
– Institute of Research in Agricultural Sciences		Lima	69
La Molina Agrarian National University	Public		
– Cooperative Program of Research in Corn (PCIM)		Lima.	3023
– Program of Research in Legumes		Lima.	445
National University of Central Peru	Public		
– Program of Research in Legumes		Junín	1244
– Program of Research in Andean Crops		Junín	340
– Program of Research in Andean Roots and Tubers		Junín	1105
– Program of Research in Cereals		Junín	108
San Antonio De Abad Del Cusco National University	Public		
– Center of Research in Andean Crops (CICA) – Program of Quinua and Kiwicha		Cusco	2000
Institution	**Sector**	**Region**	**No. of accessions**
National University of the Peruvian Amazon	Public		
– Faculty of Agronomy		Loreto	703
National University of Sanmartin	Public		
– Faculty of Agricultural Sciences		San Martín	127
– Department Agro-Silvopastoril		San Martín	82
Agrarian National University of Amazon	Public		
Germplasm Bank of Cocoa – Faculty of Agronomy		Huánuco	160
National University of Ucayali			
– Agricultural Academic Department	Public	Ucayali	69
International Center			
International Center for Research in Agroforestery (ICRAF)	Public	Ucayali	822
International Potato Center (CIP)	Private	Lima	16,958

Others			
Program for Promotion of the Exports (**Prompex)** – Legumes Project – PROMENESTRAS	Private	Lambayeque	162
Institute of Agrarian Development Lambayeque (IDAL) – Carob Project	Private	Lambayeque	3
Educational Services of Promotion and Rural Support (**SEPAR)**	NGO	Junín	198
Regional Institute for the Education and Development (REDES) – Program of Andean Crops	NGO	Junín	229
Andean Rural School (ERA)	NGO	Cajamarca	308
REGIONAL CENTER OF RESEARCH IN ANDEAN BIODIVERSITY (CRIBA)	NGO	Cusco	1221
NURSERY THE CACTUS	Private	San Martín	13
ANDEAN AMAZON RURAL ASSOCIATION (ARAA) CHOBA (CHOBA)	NGO	San Martín	196
CIVIL PARTNERSHIP MARAY	Private	San Martín	20
Total			53,327

Source: Modified from Gutiérrez and Sigüeñas (2002).

Most germplasm banks do not have the right conditions for long-term conservation of plant genetic resources. Simple constructions (brick and/or mud), and no control of temperature or humidity are predominant. Approximately, 50% of collections are kept in cold rooms at temperatures ranging from 2 to 4 °C and 40% to 80% relative humidity, for periods ranging from 5 to 10 years; the containers used are aluminum bags, glass, or plastic jars and tin containers. Some institutions such as the IPC, UNALM, and SUDIRGEB have cold rooms for the conservation of germplasm. However, an evaluation of the space and equipment capacities of germplasm banks needs to be conducted to ensure the proper conservation of national plant genetic resources.

The *in vitro* conservation of germplasm is also used as a conservation strategy. With this method, the INIA maintains collections of oca, olluco, mashua, yacon, cat's claw, cinchona, and passifloras; and, the CIP maintains 11,382 accessions for potatoes, sweet potatoes, and other Andean roots and tubers.

In relation to the conservation of animal genetic resources, there are *in situ* germplasm banks of alpacas and llamas, located at the Experimental Center of Quimsachata of the INIA in Puno. In addition, there are representative collections with samples of ecotypes of guinea pigs, which are maintained by the INIA, for research and breeding. On the other hand, the SAIS Tupac Amaru maintains the genetic nucleus of the Junin sheep breed.

The UNALM, through its Animal Breeding Program, has under its administration the National Bank of Semen, where the semen of national bulls of Holstein and Brown Swiss breeds used for livestock improvement is cryopreserved.

Despite all these efforts, conservation programs for animal genetic resources need to be implemented by including *in situ* and *ex situ* strategies for native species such as the guinea pig, creole duck, and adapted species mainly from landraces of cattle, sheep, pigs, chickens, and goats.

In situ conservation

In situ conservation of plant genetic resources in our country has been practiced since ancestral times by local farmers, especially in the Andean region. Since the 1990s, there have been many *in situ* conservation projects executed. Tapia (1998) stated that between the years 1993 and 1995, it developed a project with the aim of studying the dynamics of *in situ* conservation and establishing microgenocenters (centers of diversity) of biodiversity of Andean tubers. In addition, he noted that the Livestock Agro-Forestry Service (SESA) has registered traditional varieties of roots and tubers and has provided support for conservation in the communities of the microbasin of the rivers Jequetepeque and Cajamarca, in the Cajamarca region. In addition, the NGO, Jorge Basadre, has supported peasant organizations called ronderos to conserve their genetic material in the Chota and Cajamarca regions.

The same author, reported that the NGO, Aspaderuc, supported by the Consortium for Sustainable Development of the Andean Ecoregion (CONDESAN), has developed a project to support *in situ* conservation carried out by the peasants of the Encañada district of the Cajamarca region. They have developed a database of 254 peasants who took part in 10 seed trade fairs, which belong to 98 hamlets in the towns of Encañada, Namora, and Sorochuco, and also have registered a detailed record of more than 500 entries from tubers, grains, vegetables, fruits, and forest products.

On the other hand, an *in situ* conservation project of Andean roots and tubers was reported by the Program of Genetic Resources and Biotechnology (PRONIRGEB) of INIA (now SUDIRGEB), in the communities of Chugurmayo, La Florida, and La Victoria, in the region of Cajamarca.

From 2001 to 2006, the *in situ* Conservation Projects of Native Crops and Their Wild Relatives have been executed involving six institutions: the (ARARIWA), the Coordinator of Science and Technology in the Andes (CCTA), the Agricultural Services Center (CESA), the Research Institute of the Peruvian Amazon (IIAP), the INIA, and the Andean Project of Peasant Technology (PRATEC). The long-term goal of this project was the conservation of biodiversity in Peru, and 11 species of crops were prioritized, including several local varieties and wild relatives. It was carried out in 53 districts, which included 154 communities in 12 regions of the country. Its main activities are the conservation of biodiversity on farms, the protection of wild relatives of crops, the inventory of conservationists farms and crop varieties, the strengthening of farmers' organizations, the development of policies to support *in situ* conservation, the consolidation and development of markets for prioritized species, and the development of an information system and monitoring as an important tool for planning and coordinating conservation *in situ*.

The International Potato Center (IPC), is running *in situ* conservation projects for the crops of potatoes, sweet potatoes, and other Andean roots and tubers, in collaboration with institutions such as the INIA, the Regional Center for Andean Biodiversity Research (CRIBA)-Cuzco, the National University of Cajamarca, the Aymara Community, the UNALM, the INRENA, the Research Center of Natural Resources and Environment (CIRNMA)-Puno, and the Association for Nature and Sustainable Development (ANDES)-Cusco. The CCTA is implementing a project of *in situ* conservation in communities of the region of Huanuco, in the highlands of Peru.

In addition, since 2000, the peasant communities of Chawaytiri, Sacaca, Paru Paru, Amaru, Pampallacta, and Cuyo Grande of the district of Pisac in the Cuzco region and the Association ANDES have partnered to promote a "Potato Park". This project aims to establish a geographic area to manage their resources, including the components of the DBA, taking as a premise the valuation of local culture in the management of their resources.

The INIA through the SUDIRGEB and the Peruvian Society for Environmental Law (SPDA), in conjunction with regional governments are promoting the establishment of "agro-biodiversity zones" which are geographic areas that have high diversity and many

varieties, and knowledge associated with the management and use of these resources. These areas will prioritize the conservation and sustainable use of biodiversity by organized communities.

Documenting and systemizing genetic resources

The MINAM has developed an environmental search engine called SINIA, which allows users to search for websites of institutions related to environmental matters and biodiversity. It also examined existing information systems in the country, and has drawn up a proposal of the Information System on Biological Diversity (SINIDIB).

There is a network of Peruvian Agricultural Libraries (REBIAPE), with the National Agricultural Library (UNALM) as the focal point. In this network, there are nine associated university libraries, two documentation centers of non-governmental institutions, and the General Direction of Agricultural Information of the Ministry of Agriculture, and also other institutions that have libraries and documentation centers on topics related to agro-biodiversity.

The National Agricultural Library, the library of the IPC, and the INIA's library store a large quantity of documents related to agro-biodiversity. In addition, they edit book summaries and compact discs, and also provide search services for different national and international databases. The IIAP and the *in situ* conservation project of native crops and their wild relatives have established a library on agro-biodiversity.

Other non-governmental institutions, such as the PRATEC, the Center for Research, Education and Development (ICDE), the Center for Studies and Promotion of Development (DESCO), the Action Network Alternatives for Agrochemical Use (RAAA), and the SPDA, have documentation centers and bibliographic information services on watershed management, conservation of native crops in general, and on agro-biodiversity. The CCTA has established a Center of Information Technology (CENITEC), which operates in Lima as feeders of information to a network of local Centers for Information Technology (CINTEL) Network, which reaches its NGO partners.

Regarding information on genetic resources, the SUDIRGEB of the INIA has developed an information system using the Linux platform and free software (PHP and MySQL) for information management of its germplasm bank, which will be available on a website. The system is currently in the test phase. In addition, the INIA has been included as the Peruvian

institution where the information system of the genetic resources of Global Green will be implemented; this system is being developed by Biodiversity International and the United States Department of Agriculture (USDA) with support from the Global Crop Diversity Trust.

The *in situ* conservation project of native crops and their wild relatives has developed an information system for monitoring the *in situ* conservation; its central node is the MINAM, and the sub-nodes are being installed in institutions and organizations that participated in its execution, NGOs, and other stakeholders.

Capacity building for developing and implementing management systems of genetic resources for food and agriculture

Capacity building for the management of genetic resources involves many subjects, including policies, legislation, conservation, training, and information systems. Policies and legislation are favorable for the development and implementation of systems for managing genetic resources for food and agriculture. There are management tools, such as international conventions and treaties, regional decisions and strategies, and national strategies, laws, and programs. However, policy makers do not always recognize and properly value genetic resources, and it is necessary to complement the legal framework with the approval of the Rules of the Common Regime on Access to Genetic Resources, the sectorial rules on security of the use of biotechnology, and recognition of "agro-biodiversity areas".

Important experience was gained through the *in situ* conservation project of crop farmers and native communities, where the local organizations were strengthened, and farmers were trained in the production, processing, and marketing of their products in order to give them added value and insert them into the market.

In terms of education, many initiatives have been implemented as pilot projects, seeking to incorporate environmental issues, biodiversity, native crops, the importance of their conservation, and their nutritional value in teaching programs at the school level. Universities offer a variety of careers related to the management and conservation of genetic resources, such as biology, agronomy, livestock husbandry, forestry, and agricultural engineering. However, there are only a few related courses on sustainable use and conservation of genetic resources. At the postgraduate level, the UNALM offers a master's of Applied Ecology, Plant Genetic Improvement, and Animal Production. From 2004 to 2006, the

National Agrarian University of the Amazon (UNAS) and the Andean Project for Peasant Technology (PRATEC) implemented a master's degree in Biodiversity and Agriculture Andean-Amazon, but it was discontinued in 2007.

In addition to university studies, a realization of the thesis work in various areas related to the genetic resources has helped train young professionals and technicians, although most of them out of job in the subject of their specialization. Also, there are no specializations or refresher courses in the country for those responsible for germplasm banks.

Information systems and databases on genetic resources are still emerging; we need to strengthen such activities in order to establish a system of information on the management of genetic resources for food and agriculture at a national level and not just rely on isolated institutional efforts, which is the situation so far.

In Peru, there are various institutions and organizations that are developing activities related to genetic resources for food and agriculture, from those responsible for the coordination (MINAM), to technical institutions responsible for the conservation of these resources. These institutions, in a coordinated manner have contributed to the development of management tools for genetic resources. In addition, private institutions, such as the CIP and NGOs have developed activities on *ex situ* conservation in germplasm banks.

In this country, germplasm banks of plant and animal genetic resources exist, but in most cases do not have adequate conditions to conserve these resources in the long-term, so it is necessary to develop capabilities for long-term conservation (cryopreservation). In addition, conservation programs for animal genetic resources need to be established which encompass *in situ* and *ex situ* strategies, as well as microorganisms, and continue strengthening local organizations that conserve genetic resources *in situ* (i.e., on farms).

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Management of Plant Genetic Resources for Food and Agriculture in the Philippines: Status and Risks

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Abstract

The Philippines is home to a rich diversity of plant and animal genetic resources, and plays a vital role in preserving global species. Plant genetic resources (PGR) for food and agriculture are conserved *in situ* in national reservations and as a component of the traditional farming systems. *Ex situ* collections of important germplasm have been assembled and maintained since the early 1900s. Specific holding institutions conserve major crops in their genebanks. Most of the PGR initiatives in this country are part of the varietal improvement programs of various institutions. The status of conserving the plant genetic resources for food and agriculture, capability building and R&D initiatives are briefly discussed.

Many problems, however, beset the management of genebanks and the continued existence of some crops is put at risk. The risk factors that predispose the country's PGRs to loss or damages are categorized into natural or environmental, technical, social, and political. Most genebank managers cope with the risks on a case-to-case basis. The experiences highlighted in this report show that strengthening the capacity of holding institutions and genebank managers in PGR management should be pursued. Interagency collaboration is vital in the assessment and management of the risks to PGR conservation in order to maximize the use of physical, human, and financial resources, considering the element of quick response time and the magnitude of the risks.

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Introduction

Crop improvement and development rely on plant genetic resources (PGR) as the initial building blocks of new and improved varieties. To attain food security and agricultural self-reliance, the importance of PGR for food and agriculture (PGRFA) as sources of novel genes become even more pronounced. The value of PGR in the economy of the Philippines and the well being of the people can be gleaned from the efforts of various sectors to manage the conservation and utilization of these resources, despite the problems encountered as well as the looming threats and risks.

This report briefly presents the status of PGR conservation in our country. It highlights the problems and constraints encountered in managing PGR resources, and the ongoing PGR capability building and R&D initiatives through the intervention and/or financial support of the Philippine Council for Agriculture, Forestry and Natural Resources Research and Development (PCARRD). This paper also discusses the risk factors that predispose the PGR in selected crops to a precarious state; recent experiences in managing these risk factors are cited and depicted.

The country: Philippines

The Philippines is part of the Southeast Asian region and has a total land area of 115,830 square miles (300,000 sq. km.) that constitutes two percent of the total land area of the world. The country's 7,107 islands and islets are clustered into three groups: Luzon, Visayas, and Mindanao. Of these, Luzon and Mindanao comprise the two largest islands with land areas of 105,000 and 95,000 sq. km., respectively. Together, they represent two-thirds of the total land area of the country. Climate is tropical, characterized by relatively high temperature and humidity, and abundant rainfall. The combination of complex geological origins, fragmented layout, varying exposures to shifting winds and typhoons, and peculiar rainfall distribution has given rise to the existing complex mix of ecosystems and habitat types in this country.

Population is high (89 million) and unevenly distributed throughout the islands due to geographical, historical and social forces and to the uneven development in various regions

of the country. This distribution affects the degree of exploitation of natural resources, and the utilization of PGR.

Its archipelagic character has given the country extensive territorial waters (679,800 sq. km.) and the longest discontinuous coastline in the world. Forest zones account for about 15 million hectares (M ha.) or half of the country's total land area. The agricultural crop areas occupy about 12 M ha. These different marine, aquatic and terrestrial ecosystems harbor a rich diversity of plant and animal genetic resources.

Status of PGR for food and agriculture

The Philippines is one of the biologically richest in the world, with about 52,177 unique species of plants, animals and other life forms. About 67% of these species are endemic and cannot be found elsewhere in the world. Approximately 15,000 plant species have been so far identified within its borders. About 40% of the 8,120 species of flowering plants are endemic to the Philippines. More than 3,000 plant species in the country are used for food, medicine, fiber, essential oil, commercial timber or ornamentals (Altoveros and Borromeo, 2007). However, only about 6% of its natural vegetation remains, and 499 species are listed in the 2004 International Union for Conservation of Nature (IUCN) Red List of Threatened Species (DENR, 2005). Of this number, more than half of the species are plants. Thus, as a mega-diversity country and a biodiversity hotspot, the Philippines plays a vital role in preserving global species.

Crops in the Philippines are ranked in importance according to their contribution to food security, livelihood, and foreign trade. Rice and maize, the main staple crops, are considered the two most important crop commodities of the country. Next in importance are coconut, sugarcane, banana, Manila hemp, and mango, which are important both for domestic consumption and foreign trade.

There are wild plant species essential to food production in the country that have contributed significantly to diversification of agricultural systems. Many of these species are components of forest ecosystems, and the plants are gathered from the forest and buffer zones. However, there are no *in situ* conservation programs *per se* on specific wild plant genetic resources for food and agriculture. Wild species useful for food and agriculture that exist within the 65 protected areas under the National Integrated Protected Area System (NIPAS) are likewise protected and conserved by *fiat* (Altoveros and Borromeo, 2007).

Mangifera, Citrus, Garcinia, Nephelium, Durio, Artocarpus and *Dioscorea* are some examples of these wild species.

PGRFA are conserved *in situ* in national reservations and also as a component of traditional farming systems, such as agroforest/homestead gardens, multi-storey farming system, integrated farming system, diversified conservation farming in sloping lands, or multi-cropped home gardens.

Ex situ collections of important germplasm have been assembled and maintained since the early 1900s. There are 45 government and non-government organizations that hold *ex situ* germplasm collections in the Philippines and a list of these holdings is available only for 40 institutions (Table 1). These collections, totaling 173,205 accessions, are maintained either as seeds, living plants, or *in vitro*. A total of 40% of the total collection has been characterized morphologically, 7% on biochemical properties, 3% on molecular properties, and 60% had been evaluated for insect pest and pathogen reaction, physiological and abiotic stress reaction, and product quality. A list of the germplasm holdings for 40 institutions is available.

Table 1. List of agencies in the Philippines holding germplasm collections and number of accessions held.

AGENCY/INSTITUTION	NUMBER OF ACCESSIONS
BPI-BNCRDC	389
BPI-CRD	275
BPI-DNCRDC	624
BPI-LBNCRDC	884
BPI-LGNCRDC	275
BPI-NMRDC	25
BSU	306
CLSU	355
CMU	707
CODA	661
CSU	5
CvSU	14
DA-ILOILO	84
DMMMSU	254
DOA	1394
ERDB	197
EVIARC	76
IRRI	116,928
ISCAF	24
ISU	29
LAES	78
LSU	31

MMSU	6
NARC	773
NCRC	41
NPGRL	35,492
NPRCRTC	1122
NTA	414
PAES	219
PCA	224
PHILRICE	5861
PHILROOTCROPS	2013
PHILSURIN	580
PICRI	176
QSC	94
RMTU	100
SEARICE	769
SRA-LGAREC	1204
USM	227
WPU	275
National total	173,205

Source: Altoveros and Borromeo, 2007.

Specific holding institutions handle the conservation of major crops, like rice, maize, coconut, sugarcane, and banana. Genebanks of Philippines Rice Research Institute (PhilRice), Crop Science Cluster of the University of the Philippines Los Baños College of Agriculture (UPLBCA), International Rice Research Institute (IRRI), Magsasaka at Siyentista Tungo sa Pag-unlad ng Agrikultura (MASIPAG), and Southeast Asia Regional Initiatives for Community Empowerment (SEARICE) conserve rice germplasm. There are a total of over 5,500 collected and documented traditional varieties of rice in the country, and 4 wild relatives. Philippine rice diversity is attributed to the diversity of ecosystems, cultural management practices, and preferences. For maize, the National Plant Genetic Resources Laboratory (NPGRL) of UPLB – Institute of Plant Breeding (UPLB-IPB) has assembled a germplasm collection of 2,099 accessions; of this number, 389 accessions are farmers' varieties collected from 32 maize growing provinces all over the Philippines. For coconut, the Philippine Coconut Authority (PCA), Visayas State University (VSU) and UPLB hold the germplasm collections, with PCA having national mandate and, thus, the largest collection totalling 264 accessions. In the case of Manila hemp or abaca, there are 773 accessions in one *ex situ* collection in the country, consisting of traditional cultivars or landraces, wild

types, breeding lines, and improved cultivars. Only in our country can such diversity in Manila hemp be found.

However, the existence of these crops has faced various threats. In rice, destruction of the natural habitat threatens the continued existence of the natural populations of wild rices. In white and yellow maize, the country's traditional or "native" farmers' varieties have evolved over four centuries of continuous cultivation and may possess many desirable characteristics and adaptations. But these varieties are threatened by replacement of traditional varieties with commercial hybrids. The same is true for banana, which is threatened by the replacement of wild types with cultivated species to increase income. Another threat is the destruction of wild bananas during shifting cultivation, road construction, and roguing. Abaca is further threatened by overexploitation/overharvesting of natural stands as well as land use change. Occurrence of destructive pests and diseases, as well as natural calamities, and the use of a few genotypes contribute to the rapid loss of banana and abaca germplasm. Present stands of the wild type coconuts are endangered by the replacement of wild types and traditional varieties with recommended ones. Likewise, cutting of mature and productive palms pose serious threats to this crop and the industry in general. In mango (*Mangifera indica*) the predominance of only one variety ('Carabao') threatens the existence of minor varieties; and the replacement and cutting down of trees, as well as land use change and habitat destruction, are other threats. In the case of coffee, outbreaks of coffee rust have decimated coffee populations all over the country. There are still pockets of the traditional coffee populations remaining, but most of the varieties currently grown are introductions.

PGR capability building and R&D initiatives

The importance of PGR, in terms of value and use, needs to be promoted so that the public can better participate in their conservation and wise utilization. Toward this end, strengthening the capacity of holding institutions and genebank managers in PGR management has been relentlessly pursued. Moreover, support to PGR-related R&D projects is given priority by PCARRD-DOST under the national science and technology agenda.

Through a survey in 2002 among national agriculture and resources research and development system (NARRDS) institutions conducting PGR-related activities, the UPLB-NPGRL noted that these institutions have a core of staff with scientific training in the agricultural and biological sciences. However, PGR, as a growing field of specialization, requires staff with specific skill and competence, and specialized training on the different aspects of PGR conservation, management and documentation is needed to retool the staff. To address this need, for the past three years, a series of non-formal training courses benefiting 75 researchers nationwide were conducted on the following areas: PGR conservation and management, PGR documentation and information management, and PGR characterization using standard descriptors. A training on PGR valuation for 50 researchers is scheduled in the last quarter of this year.

The Department of Science and Technology (DOST) funds ongoing and new initiatives related to PGR R&D, through the active participation of PCARRD as coordinating and monitoring council. Six PGR-related projects are being implemented by nine different state universities and colleges, Department of Agriculture agencies, and one private foundation. These R&D projects focus on the conservation and utilization of tropical fruits, indigenous orchids, abaca, chickpea, and selected crops with local and international market potential.

The project on collection, conservation, regeneration and re-introduction of indigenous orchids in selected protected natural habitats aims to conserve the indigenous biodiversity of Philippine orchid species, regenerate a portion of the conserved biodiversity through in-vitro culture to produce living orchid plants in quantity, and reintroduce the regenerated diversity of selected species into protected natural habitats. Additional diversity of indigenous orchid species will be collected as seeds in fruit capsules from provinces not covered by the first phase of the project. Selected exportable agricultural crops are being evaluated for adaptability, productivity and optimum growth, and their utilization promoted to interested clientele in a private sector-led project on collection, evaluation and utilization of exportable agricultural products.

A new project on safekeeping crop diversity in the national germplasm repository regenerates and multiplies the seed germplasm collections, rehabilitates the field genebank and assures continuous safekeeping of the germplasm. These objectives will be achieved by complementing the field genebank with other strategies, such as *in vitro* conservation or by maintaining the germplasm inside the greenhouse/ nursery. Regeneration was completed for 100 accessions each of corn, sorghum, tomato, eggplant and pepper. The seeds harvested

were all processed and stored in the seed genebank. For the field collections, 557 accessions have been rejuvenated and rehabilitated. These include mango, chico, jackfruit, citrus, *Syzygium* spp, pili, cashew, *Musa balbisiana*, and other botanical collections. I*n vitro* collections involving 403 accessions of edible *Musa*, *Musa balbisiana*, sweet potato, taro and yam were maintained in the tissue culture laboratories.

Conservation and use of tropical fruit species diversity in the Philippines is a foreign-assisted project that aims to establish and enhance genebanks of priority fruit species including their wild relatives; develop and make available database of germplasm holdings; identify elite accessions of priority species for further evaluation; and strengthen capabilities of participating institutions on PGR conservation and management. This project involves fruit species, such as: *Canarium ovatum* (pili), *Garcinia mangostana* (mangosteen) and other *Garcinia* species, *Durio zibethinus* (durian), *Artocarpus heterophyllus* (jackfruit), and their related species.

Two newly approved projects deal with chickpea and abaca. The project on introduction, evaluation, development of package of technology and promotion of chickpea (*Cicer arietinum* L.) in the Cordillera Administrative Region shall collect and characterize chickpea accessions, select outstanding entries and evaluate them in the lowland and upland conditions of CAR. A package of technology for chickpea production and chickpea-based processed products will also be developed. Coupled with promotion through demo farms and field days, the project hopes to facilitate the adoption of chickpea in the CAR and lessen the country's dependence on importation of this commodity. On the other hand, the project on national multilocational trials of promising abaca bunchy top resistant genotypes shall evaluate the performance of promising disease-resistant abaca varieties/hybrids in different abaca bunchy-top disease - infected abaca areas in the country, and identify stable high-yielding and disease-resistant genotypes that can be released to farmers in all major abaca-growing areas.

Further capacity building and research initiatives are needed towards increasing awareness on the importance and value of PGRFA, using modern approaches to genetic diversity assessment, monitoring of genetic erosion, and assessment and management of risks to PGRFA.

Problems and constraints in managing PGR

Many problems beset the management of genebanks, foremost of which is funding. Most of the PGR initiatives in the country are project-based, and the activities on collecting, characterization and conservation are part of an institution's varietal improvement programs. The lack of full government and institutional financial support results in incomplete and fragmented efforts in collecting, characterization and conservation of PGR. Inadequate funding affects the entire management spectrum, from personnel, facilities, to number of accessions maintained or size of collections.

There are other problems and constraints commonly encountered but genebank managers devise practical solutions to address them. Some of these problems and solutions employed are:

- Costly conservation of germplasm collection in field genebank, cold storage and in vitro culture particularly with regard to highland crops or semi-temperate crops – Possible duplicates were identified to reduce the number of accessions maintained.
- High risk of loss especially in field genebank – Only those with potential traits for utilization are maintained in the field genebank/propagation block. Duplicates were deposited in other genebanks, e.g. in the case of the NPRCRTC, duplicates are with the NPGRL, UPLB, and PRCRTC, VSU.
- Limited/Lack of fully trained personnel/staff for proper characterization, duplicate identification, conservation and maintenance of germplasm collection, and databank manager to handle different kinds of data about germplasm collection, conservation, and utilization – Training of researchers on descriptor development, characterization, conservation, and as genebank curator.
- Limited facilities and equipment for *in vitro* conservation and propagation of germplasm – Only those with potential use are conserved in-vitro; Duplicates were deposited in other genebanks.
- Lack of equipped cold storage facilities for short, medium and long-term storage of germplasm – Seeds of annual vegetable crops are also deposited in UPLB-NPGRL seed storage.

These problems, *per se*, pose a challenge to the sustainable conservation of genetic resources and contribute in part to a genebank's predisposal to risks, as these are a function of vulnerability and capacity.

Risk factors in PGR management

Ong, *et al*. (2002) cautioned that every parcel of land that is converted, cultivated, or developed will likely result in the loss of unique life forms found nowhere else on the planet. Thus, any change in land use poses a risk to the existing biological resources. There is a high rate of biodiversity loss, damage or injury due to high commercial and social demand, and the biodiversity is under constant threat of extinction from over-harvesting or over-collection, pollution, widespread land conversion, urbanization, burgeoning population, and poverty.

In general, the risk factors that predispose PGRs to loss or damage may be categorized into either natural or environmental, technical, social and political; however they are also inter-related and there are cases when their overall impact is aggravated by the combined effects of individual risk factors.

Some of our country's experiences on the risks encountered and the actions taken to mitigate their adverse effects or provide rehabilitation to the damage done are cited and depicted.

Natural or environmental

No matter how well managed a genebank is, when major natural perturbations and disaster strike, the effects on the stored germplasm are catastrophic and may be permanent. Natural calamities often resulting to disasters in southeast Asia include the occurrence of strong typhoons, extreme climatic events such as El Niño and La Niña that bring about long periods of drought and floods, tsunamis, earthquakes, fires, landslides, and volcanic eruptions (SEARCA, 2008). Approximately 27% of the country is vulnerable to drought (DENR, 2005), alternating with floods and typhoons yearly. An average of 19 typhoons per year pass the archipelago from June to December.

- PCARRD has recently released funds to rehabilitate the national genebank at NPGRL because typhoon 'Milenyo' (international code name Xangsane), which had a velocity of 190kph, severely damaged the NPGRL genebank building and facilities in 2006.

Two-meter high mud and floodwater damaged the service units located at the ground floor of the building, including the seed research, morpho-anatomical and germplasm documentation units, the greenhouse for asexually propagated germplasm, and damaged equipment and materials including airconditioners, dehumidifiers, standby generators, and vehicles. About 70% of the genetic materials (350 accessions) stored in the NPGRL were damaged by floodwaters and mud, while 100% of the laboratory's root crop collections were buried in mud, and about 5% of the laboratory's total seed collections were also damaged. The typhoon rendered inoperative the four convirons or cold storage facilities, without which the germplasm lose long-term viability.

- The International Rice Research Institute (IRRI) then came to the rescue by temporarily storing the medium-term germplasm collections of major Philippine agricultural crops. Likewise, the Global Crop Diversity Trust funded the restoration of the genebank, in coordination with Bioversity International, through the International Network for the Improvement of Banana and Plantain Asia Pacific Office. Seed collections such as peanut, sorghum, and maize were repacked and sealed into air and water-tight aluminium foil envelopes. A dehumidifier and two power saws were purchased; two dehumidifiers, two screenhouses, the fruit crops nursery, air conditioning and compressors for the cold storage rooms, and a stand-by generator were repaired. Furthermore, the vegetative root crop, fruit crop, banana, taro, and sweet potato collections were rescued and moved into safer conditions. Unfortunately, parts of the collection were not duplicated anywhere else, and consequently many varieties have been lost forever.
- Other ways by which genebank managers pre-empt the risk from such natural calamities is by yearly rejuvenation of germplasm in field genebank, although this is subject to availability of funds. Another is by a system of repatriation/ reintroduction of traditional/farmers' varieties for re-establishment of the ecosystem.
- PCARRD recently approved a project on safekeeping crop diversity in the national germplasm repository by regenerating seed collections and rehabilitating and rejuvenating the germplasm in the field genebank. Continuous safekeeping of the germplasm is assured by complementing field genebank with other complementary strategies (i.e. *in vitro* conservation, maintaining the germplasm inside the greenhouse/nursery).

- On the other hand, those damaged by lightning and bush fire were totally replaced, as in the case of the coconut germplasm in Zamboanga. Another case is the first large fire in the dipterocarp forest that occurred in 1983 in the southern part of the country, Mindanao; that incident resulted in near loss of the valuable mossy forest and its biodiversity-rich vegetation. These fires were induced by the prolonged drought attributed to the El Nino phenomenon.

Technical

1. Pest infestation and disease infection – Examples in the past when an early warning system would have mitigated the destructive effects of pest and disease outbreaks are in the case of ring spot virus in papaya that caused the collapse of the local papaya industry; mosaic and bunchy top viruses that threatened the erosion of banana and abaca diversity; tristeza virus that wiped out citrus genotypes; and the black bug infestation in rice. Yearly rejuvenation of germplasm in field genebank is a way to address this concern. But there is a need to devise a system or mechanism for early warning, especially in reference to pest and disease epidemics. Corollarily, failure to detect and quickly remove diseased sample collections poses a risk. Thus, having trained personnel is essential.
2. Insufficient safety duplication – For security of stored material there are some duplications in other genebanks, but these are not sufficient. Examples of collections that are duplicated in other genebanks are rice, banana, mango, sweetpotato, Manila hemp, and coconut. Except for rice, seed collections are poorly duplicated. Insufficient safety duplication is also the case in medicinal plants, some tropical fruits and nuts, and industrial crops. Meantime, some institutions do yearly rejuvenation of germplasm in field genebank; another way is by a system of repatriation/reintroduction of traditional or farmers' varieties for re-establishment of the ecosystem.
3. Loss of information due to inadequate or wrong documentation – A survey by NPGRL found that record books (88%), data sheets and computers are the most common means used for documentation in our country. About 69% of the holding institutions have computers that can be used for documentation, but these are not fully dedicated to their PGR unit. In the institutions with computers, only 22 (54% of total) have their data encoded, and 19 (46%) have not yet encoded their germplasm data. Only four out of 44 institutions have their own database management systems. The other

institutions have their data recorded manually. Some do not have written data; the information about their collections is kept mentally by the researchers. In some institutions, basic information about the collections is lacking, specifically passport data such as the place of collection, acquisition date, local name, and pedigree. Retrieval of information about their collection may be tedious and some vital information is therefore lost.

4. Failure to collect genetic material and capture *in situ* genetic diversity before it is lost – Factors such as urbanization, land use change and climatic events, agricultural intensification and the replacement of traditional varieties with modern ones can result in loss of the genetic material before it is collected, characterized and conserved.

5. Inadequate/poor storage facilities – Only 4 of the institutions that conserve by seeds have cold storage rooms. In the absence of cold storage rooms, several institutions maintain their seeds in air-conditioned rooms, chest freezers, or under ordinary room condition. Of the 48 different institutions, 17 have tissue culture laboratories conducting normal growth conservation and micropropagation. Of the 17, only 5 are employing slow growth conservation. Only one institution conserves germplasm by pollen, and this is used primarily for its breeding program.

6. Absence of established methodologies for assessing plant genetic erosion – The threat of genetic pollution or introgression, either from genetically modified organisms (GMOs) or from conventionally bred crops to wild species, has become an increasing potential risk to the *in situ* genetic conservation of crop wild relatives.

Social and political

1. Theft and organized pilferage – Fencing of field genebank or provision of security guard in the experiment station/fields become a necessity especially in cases when theft is rampant. Security operation was intensified and assistance sought from local government units to contain organized pilferage in the genebank.

2. Unstable peace and order situation arising from conflicts, especially in Mindanao – Duplicate collections were established in other institutions.

3. Urbanization – Establishment of the Zamboanga City Free Port and Economic Zone resulted in a request for additional area which will greatly damage the areas covered by the *ex situ* coconut collection. Construction of new roads and road widening

resulted in the boling and/or transferring of all affected palms. – Duplicate collections were established in other institutions.

4. Quarry operations, e.g. the rivers inside the coconut genebank, damaged river banks, as well as road networks have affected the coconut plantations where the coconut accessions are located.

In addition, changes in the relative importance of major crops in the country influence the prioritization for conservation of those crops. These changes can be attributed to the following factors: land conversion, increase in volume of export due to increased global demand, pests and diseases, expanded use and new markets, importation and competition with locally-grown crops, or rehabilitation programs. Corollarily, valuable genetic resources not yet collected and preserved may be endangered by these changes in land use.

For now, most genebank managers cope with the risks on a case-to-case basis. The methodologies for assessing these risks and the mechanisms for preparedness need to be addressed, prioritized and included among the capacity building and R&D efforts of PGR management. In the Philippines, there has been no systematic assessment of genetic erosion of PGR (Altoveros and Borromeo, 2007). There is no early warning system yet for threats to PGR, particularly the agrobiodiversity in the country, and mechanisms for preparedness in handling the risk factors need to be explored. For introduced species, the National Committee on Biosafety of the Philippines has formulated the guidelines for the conduct of risk assessment and biosafety. Interagency collaboration would be vital in managing the risks to maximize physical, human, and financial resources, considering also the element of quick response time.

High probability of success and sustainability of PGR conservation efforts, especially amidst the threats and risks at hand, can only be assured by good management at all levels (local, national, regional), institutionalized mechanisms and structures, and strong sustained support from internal and external sources.

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The Status of Conservation, Utilization, and Risk Management of Genetic Resources in Taiwan

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Abstract

Genetic resources may be used through complementary *ex situ* and *in situ* conservation approaches organized at the regional, national, and/or global levels. Genetic resources as defined in the *Convention on Biological Diversity* (CBD) refer to physical, tangible genetic materials as well as genetic information and knowledge. Five major germplasm conservation projects covering crops, forests, aquaculture, livestock, and microorganisms have been carried out at national institutes in Taiwan. The Plant Genetic Resources Center was established at the Taiwan Agricultural Research Institute in 1993. To September 2008, seed collections of 69,319 accessions are being conserved in long- and medium-term storage rooms. In field genebanks, collections and preservation of germplasm of fruit trees and medicinal plants include approximately 4968 accessions and are being maintained in several repositories. In total, 1745 accessions of clone germplasm collections are being cultured *in vitro* in tissue culture rooms. In addition, so far, more than 61,249

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accessions of genetically modified (GM) rice T_1 seeds and 32,799 accessions of T_2 seeds have been processed and conserved in a genebank. These seeds are available to distribute to scientists/ researchers for phenotypic screening or functional genomic research. The Tree Seed Bank was established by the Taiwan Forestry Research Institute in 1956. It conserves orthodox seeds of woody plants collected from natural forests for the perpetuation of seed stocks of 47 families, 151 species, and more than 700 seed lots. The conservation of farm animal genetic resources project was established by the Taiwan Livestock Research Institute in 1987 for further utilization of local breeds in the animal sector. New and emerging technologies, such as DNA library of local breeds, are being applied to reveal the genetic basis of disease resistance, adaptation to environmental stresses, and production efficiency. Capacity building for risk management of animal cells and/or tissues in cryopreservation banks with liquid nitrogen preservation has been in operation since 2005 to preserve valuable samples of fish and other aquaculture and fisheries species and wild relatives of livestock. Tilapia is one of the most important cultured freshwater fish species economically in Taiwan. In order to maintain its genetic variability and diversity, *in situ* bio-banks for stock breeds and conservation of tilapia and other aquacultured fish in culture systems were established by the Freshwater Aquaculture Research Center of the Taiwan Fisheries Research Institute in 2005.

Capacity building for management of germplasm described in this report is a key to stimulating sustainable utilization of genetic resources, especially local varieties/breeds. Action plans on risk management, safety conservation, species identification, hybridization, and commercial utilization of genetic resources for food and agriculture have been formulated to develop markets for biodiversity-based products. Efficient management of genetic resources is essential to ensure the present and future security of food and agriculture. As a participant in global efforts to conserve genetic resources, we expect greater benefits and responsibilities. Particularly, in term of global climate change and food crises, actions are needed to equip and manage genetic resource conservation systems as an effective component of national and international food and agriculture security.

Introduction

Taiwan is located along the boundary between the tropical and subtropical zones and is rich in biodiversity and ecological habitats. Although its areal extent is quite small, the biodiversity resources in Taiwan are extremely abundant, and there are diverse ecosystems due to the excellent geographical features and topographical environments. At present, there

are at least 6000 species of plants known in Taiwan, accounting for 2.1% of all plant species in the world, while at least 10,000 species of microorganisms have been recorded, accounting for 8.6% of the world's total, of which 2% are known to be endemic fungal species. Hence important questions concern how to more deeply understand characteristics of various ecosystems in Taiwan, how to better manage ecosystems, how to enhance the conservation of biodiversity, and how to sustainably utilize natural resources. These are the challenges currently facing the country and thus, are the main focus of technological development. Moreover, the rapid growth in agricultural production and economic development in recent years resulted in drastic reductions in the native flora of Taiwan. The genetic base of fundamental crops was narrowed by rapid progress in plant breeding and the large-scale adoption and frequent turnover of improved cultivars.

Genetic diversity refers to natural resources which are valuable and important global resources. Germplasm is indispensable material for the continued development of bioresources for food and agriculture in Taiwan. Agricultural scientists, including plant breeders are eager to use resources such as germplasm to improve crops. In view of the long-term needs of ecosystems, the sustainable conservation and utilization of genetic resources have drawn the attention of scientists and governments of all countries. To meet these increasing demands for genetic stocks and at the same time, to address concerns about the serious loss of biological resources, many nations have established genebanks to conserve and utilize plant genetic resources for food and agriculture.

Establishing national genebanks

At present, the focus of research and development on bioresources is on “the establishment of national germplasm banks” and “the effective management and utilization of bioresources”. To meet both national and global needs, the relevant institutes must recognize and act on the needs of the nation’s germplasm collections and conservation. Thus, five major germplasm conservation projects concerning crops, forests, aquaculture, livestock, and microbial genetic resources have been carried out at national institutes in Taiwan. These projects include a national system of collecting and conserving germplasm, evaluating native species, local species, and species related to folk use, as well as research on developing technologies for conservation, identification, and utilization. These are needed to establish an integrated national system of biological germplasm conservation and utilization, and ensure that bioresources can be sustainably managed and used.

Agricultural improvement depends on the utilization of abundant plant genetic resources and the carrying out of scientific research. Plant germplasm is indeed the basis of crop improvements and genetic variations, and biodiversity is the driving force for continued progress in plant breeding. The cultivation of hybrids and fixed commercial varieties has threatened the survival of indigenous varieties and wild plants. These primitive types may be genetically resistant to diseases or tolerant of environmental stresses and are considered to be precious sources of germplasm for utilization in the future.

Taiwan has realized the importance of sustainable conservation and utilization of plant genetic resources. The Plant Genetic Resources Center (PGRC) was established at the Taiwan Agricultural Research Institute (TARI) in 1993. The Center is administered by the TARI under supervision and funding by the government.

Collections and conservation of plant germplasm

Activities at the PGRC can be divided into four parts: collection, preservation, distribution, and research on the preservation and identification technologies of plant genetic resources. Germplasm collections include plants maintained in greenhouses and field plantings, dried seeds stored in sealed envelopes at low temperatures, and *in vitro* cultures of plant tissues and buds. The targets of collection include germplasm currently stored in seed units within the country, new varieties developed from breeding programs, genetic materials acquired from international exchange, and germplasm collected by exploration teams. Imported germplasm materials must be examined by the Bureau of Animal and Plant Health Inspection and Quarantine (BAPHIQ) for quarantine purposes to ensure importation of pest-free and viable materials for reproduction and distribution.

The methods for preservation of collected germplasm are based on the type of material: seed or non-seed (clonal materials). Seeds are the most commonly preserved form of germplasm. According to the level of seed tolerance to low temperatures and desiccation, seeds are further divided into storable and non-storable types. The majority of seeds of cereal grains, legumes, and vegetable crops can be stored for long periods of time under conditions of low humidity and low or subfreezing temperatures.

The conditions of storage rooms for long-, medium-, and short-term storage are –12±2 °C and 40%±3% relative humidity (RH), 1±2 °C and 40%±3% RH, and 10±2 °C and 40%±3% RH, respectively. Collections in long-term storage rooms are only preserved to regenerate fresh seeds and are periodically examined for seed viability. The main purpose of this storage

is for the perpetuation of seed stocks. The life expectancy of seeds preserved in long-term storage at this Center is between 30 and 50 years. The collections in medium-term preservation are for seeds that are actively used for distribution, exchange, multiplication, and evaluation. The seeds are also used to supply the base collection in long-term storage. Regular germination tests and seed regeneration are required for materials in storage in order to maintain seed viability and sufficient quantity. The short-term storage room is provided for storing breeder's working materials such as lines, parents, and progeny.

By September 2008, 76,032 accessions had been stored in long- and medium-term storage rooms, tissue culture rooms, or field repositories at the PGRC. These accessions represent 181 families, 703 genera, and 1071 species of plant germplasm. These seed collections include 31,832 accessions in the long-term storage room and 69,319 accessions in the medium-term storage room (Table 1). For the field genebank, collections of germplasm including fruit trees, medicinal plants etc., of approximately 4900 accessions are being grown and maintained in several repositories. In total, 1745 accessions of clonal germplasm are being preserved and cultured *in vitro* in tissue culture rooms at the TARI.

Table 1. Accessions of seed collections preserved in the PGRC in 2008

Crop	Scientific name	Passport data	Character data
Soybean	*Glycine max*	19,153	7438
Rice	*Oryza sativa*	7584	7760
Tomato	*Lycopersicon esculentum*	6860	124
Mungbean	*Vigna radiate*	6586	5000
Pepper	*Capsicum annuum*	3581	364
Eggplant	*Solanum melongena*	3120	470
Peanut	*Arachis hypogaea*	2124	1479
Common flax	*Linum usitatissimum*	1811	0
Sugarcane	*Saccharum officinarum*	1397	590
Asparagus bean	*Vigna unguiculata*	1338	258
Sweet potato	*Ipomoea batatas*	1321	596
Corn	*Zea mays*	1106	313
Lettuce	*Lactuca sativa*	706	0
Snap bean	*Phaseolus vulgaris*	617	147
Edible amaranth	*Amaranthus tricolor*	591	0
Sorghum	*Sorghum bicolor*	578	492

(Continued)

Black gram	*Vigna mungo*	538	0
Chinese cabbage	*Brassica campestris* Pekinensis group	536	0
Cucumber	*Cucumis sativus*	494	48
Spinach	*Spinacia oleracea*	417	0
Watermelon	*Citrullus lanatus*	403	67
Tobacco	*Nicotiana tabacum*	385	0
Muskmelon	*Cucumis melo*	343	177
Adzuki bean	*Phaseolus angularis*	286	245
Bitter melon	*Momordica charantia*	269	122
Cauliflower	*Brassica oleracea Botrytis group*	262	1
Peach	*Prunus persica*	260	183
Bottle gourd	*Lagenaria siceraria*	252	68
Jute	*Corchorus capsularis*	246	0
Luffa	*Luffa cylindrical*	242	225
Banana	*Musa* spp.	232	88
Snow pea	*Pisum sativum*	225	79
Chinese mustard	*Brassica campestris* Chinensis group	214	11
Chinese kale	*Brassica oleracea* Alboglabra group	206	109
Asparagus	*Asparagus officinalis*	205	100
Garlic	*Allium sativum*	204	214
Squash	*Cucurbita moschata*	203	49
Mango	*Mangifera indica*	183	22
Sunflower	*Helianthus annuus*	166	125
Mustard	*Brassica juncea*	166	20
Radish	*Raphanus sativus*	163	15
Taro	*Colocasia esculenta*	132	34
Buckwheat	*Fagopyrum esculentum*	128	0
Tea	*Camellia sinensis*	102	101
Wax gourd	*Benincasa hispida*	102	22
Others		7283	1455
Total		73,320	28,611

Genetically modified (GM) rice germplasm

Technologies of gene knockout and activation tagging have been developed, and they provide a direct route to determine the function of a gene. T-DNA insertion mutagenesis is one of the most popular methods for elucidating gene functions. Transgenic rice carrying T-DNA is being generated at Academia Sinica. Transgenic rice seeds carrying T-DNA are being produced at the TARI and preserved at the PGRC, TARI to ensure their quality and viability. At present, more than 61,249 accessions of rice T_1 seeds and 32,799 accessions of T_2 seeds have been processed and conserved in the genebank. These seeds are available to distribute to scientists for phenotypic screening or functional genomic research.

Clonal germplasm

For several reasons, germplasm of some crops cannot be stored as seeds. In such cases, germplasm must be maintained as live plants in the field or under cover (e.g., greenhouses or screenhouses), or as pollen, tissue cultures, or cuttings (e.g., scion wood of fruit and nut trees). Many clonal materials such as potatoes, sweet potatoes, yams, taro, strawberries, and some ornamental plants are cultured on artificial media in tissue culture (TC) room. TC allows rapid clonal propagation of a large number of plantlets over a short period, as well as maintenance of germplasm under controlled conditions in small spaces and with reduced labor requirements. TC techniques are space-saving and more intensively managed than techniques of field plantings. TC also ensures production of pathogen-free plants. Moreover, these materials are also desirable for international shipment and germplasm exchange.

At present, the TC room of the PGRC has preserved 810 strains of asexual reproductive germplasm, including 379 strains of sweet potatoes, 22 strains of potatoes, 17 strains of yams, 36 strains of taro, 16 strains of strawberries, 177 strains of lilies, 63 strains of chrysanthemum, seven strains of *Anthurium* of the Araceae, two strains of *Anoectochilus*, 74 strains of bananas, 15 strains of herbs, and one strain each of *Buplerum* and *Astragalus membranaceus*. They are all preserved in MS medium, at 20 °C, under 12 h of light and subcultured periodically depending on the species of plant.

Field genebanks

Germplasm materials such as fruit trees, potatoes, sweet potatoes, bananas, orchids, and medicinal plants are grown in seven repository gardens at different elevations and latitudes for conservation in various environments in Taiwan. The field genebank for preservation of vegetatively propagated crops is separately located in various agriculture institutes/organizations with major purposes of germplasm inspection, quarantine, nursery reproduction, and education about bioresource conservation. Total collections of the fruit tree repository include 45 families and 88 genera in about 800 accessions. In this repository system, tropical/subtropical fruits such as apple, plum, peach, pear, Chinese apricot, persimmon, grape, loquat, pineapple, longan, litchi, citrus, avocado, passion fruit, banana, papaya, mango, Indian jujube, star fruit, guava, wax apple, mulberry, and some exotic fruits are preserved in field genebanks (Table 2). The collections of medicinal plant germplasm preserved in field genebank include 23 species of ferns, one species of gymnosperm, 880 species of dicotyledons and 114 species of monocotyledons, among which 109 species are endemic to Taiwan.

Table 2. Germplasm materials of fruit trees grown in field nurseries for conservation

Repository garden	Preserved crops	No. of accessions
Wanshiang high-elevation field repository	apple, peach, pear	72
Loona middle-elevation field repository	peach, plum, Chinese apricot, persimmon	240
Wanfeng (TARI) low-elevation repository	grape, loquat, peach, plum, Chinese apricot, persimmon	178
Chiayi tropical and subtropical repository	pineapple, longan, litchi, citrus, avocado, passion fruit, banana, exotic fruits	596
Fengsan tropical repository	papaya, mango, Indian jujube, star fruit, guava, wax apple	311
Guansih citrus repository	citrus, pomelo	112
Kukeng field repository	tropical and subtropical fruit crops and woody flowering plants	13
Miaoli Agricultural Research and Extension Station	mulberry	138
Field nurseries at other places	fruit crops, medicinal crops, and others	3446
Total		4968

Seed regeneration

In order to maintain sufficient quantities and quality of seeds in genebanks, regeneration and characterization of the collected materials are carried out at TARI headquarters and by participating farmers and other collaborating institutes. Standardized procedures of seed regeneration are used. Regeneration procedures are based on standard protocols that take into consideration the breeding structure of each species in order to preserve the genetic integrity of the original population in the regenerated materials. In seed genebanks, the risk of introducing foreign genes or materials can occur anytime a seed sample is handled. Extensive care is taken during seed regeneration and processing with complete inspection and cleaning of all equipment used between accessions. These standard operating procedures continue throughout the storage and distribution processes to prevent admixing of seeds.

Cryopreservation

Plant germplasm stored in or suspended above liquid nitrogen at –150 to –196 °C may greatly extend storage periods. At the PGRC, embryos, shoots, and meristem tissues of crop germplasm such as grapes, bananas, papayas, strawberries, pineapples, sweet potatoes, mountain yams, cassavas, and orchids are preserved in liquid nitrogen at an extremely low temperature (–128 °C). However, its general application to germplasm management and utilization requires considerably greater knowledge and function than currently exists as well as a more-precise understanding of the protocols and control processes of cryopreservation.

DNA genebanks

DNA contains the molecular sequences that comprise genes. Thus, an organism's isolated DNA contains all of its genes. The potential to store isolated DNA underscores the central importance of germplasm as genetic information. This technology is already becoming available. At present, the NPGRC has established a crop genetic resource conservation system with the YAC genebank; in addition to saving storage space, the preserved DNA is suitable for biotechnological research and applications. Future objectives will focus on preserving important crop germplasm in Taiwan, including important released breeding varieties of crops and native plant species with potential for further development.

Germplasm distribution

Distribution of germplasm remains one of major functions of the PGRC. Germplasm materials stored at the PGRC are not only for conservation but also to support crop research and utilization programs in Taiwan. These genetic materials are available by request for academic purposes. The germplasm is distributed free of charge, and their related information is included as well for reference. The PGRC aims to serve as a storage site for all crops of Taiwan. Through international collaboration on collection and exchange of germplasm, we also aspire to become an international genebank for tropical and subtropical crops.

Germplasm information system

A computerized information system has been completed at the PGRC to strengthen collection, conservation, and utilization of crop germplasm, and modernize management and operation of plant genetic resources. This network system is linked to other germplasm information centers around the world. Researchers and breeders can use the linked net to obtain information and request plant genetic resources on the web site at: *http:/www.npgrc.tari.gov.tw*.

Conservation of forest genetic resources

Referring to the *Flora of Taiwan* published from 1993 through 2000, there are approximately 231 families and 1314 genera with a total of 3982 species of native vascular plants in Taiwan. Totally, there are 4216 species of vascular plants including 234 species which are invasive species which have been introduced and naturalized in Taiwan. A Tree Seed Bank was established at the Taiwan Forestry Research Institute (TFRI), Taipei, in 1956. The purpose of this genebank is to conserve orthodox seeds of woody plants collected from natural forests to perpetuate seed stocks. For seeds of orchards and plantation forests, these important recalcitrant seeds of woody plants are stored in moist sphagnum at 4 °C for short-term storage (1~3 years). The temperature of the storage rooms of the Tree Seed Bank is set to –20 °C for preserving orthodox seeds, and 4 °C for recalcitrant seeds.

Activities of the Tree Seed Bank include forest seed collection, preservation, research, and distribution. Research is necessary to understand the seed storage type for short- or long-term storage and dormancy-breaking methods for seed germination in nurseries. Seeds

stored at the Tree Seed Bank are not only for conservation but also for supporting plantation, afforestation, and international seed exchanges.

Species and classification of seed stocks at the Tree Seed Bank

The Tree Seed Bank is storing 47 families and 151 species of plants, comprising more than 700 seed lots. The genera, families, and species of tree seed collections are listed in Table 3.

Table 3. Woody species of plants conserved at the Tree Seed Bank, TFRI

GYMNOSPERMAE	
CUPRESSACEAE	
1. Calocedrus macrolepis var. *formosana*	*2. Chamaecyparis formosensis*
3. Chamaecyparis obtusa	
PINACEAE	
1. Abies kawakamii	*2. Picea morrisonicola*
3. Pinus armandii var. *masteriana*	*4. Pinus elliottii*
5. Picea morrisonicola	*6. Pinus massoniana*
7. Pinus taiwanensis	*8. Pseudotsuga wilsoniana*
9. Tsuga chinensis var. *formosana*	
PODOCARPACEAE	
1. Nageia nagi	
TAXODIACEAE	
1. Cunninghamia konishii	*2. Taiwania cryptomerioides*
ANGIOSPERMAE	
ACERACEAE	
1. Acer albopurpurascens	*2. Acer kawakamii*
3. Acer morrisonense	*4. Acer morrisonense*
5. Acer serrulatum	
ANACARDIACEAE	
1. Pistacia chinensis	*2. Rhus javanica* var. *roxburghiana*
3. Rhus succedanea	
AQUIFOLIACEAE	
1. Ilex asprella	*2. Ilex formosana*
3. Ilex lonicerifolia var. *matsudai*	*4. Ilex micrococca*
5. Ilex rotunda	
ARALIACEAE	
1. Dendropanax dentiger	*2. Schefflera octophylla*

(Continued)

BETULACEAE	
1. Alnus formosana	*2. Carpinus kawakamii*
BIGNONIACEAE	
1. Radermachia sinica	
BORAGINACEAE	
1. Ehretia longiflora	
CAPRIFOLIACEAE	
1. Sambucus chinensis	*2. Viburnum foetidem*
3. Viburnum odoratissimum	
CELASTRACEAE	
1. Celastrus kusanoi	
CORNACEAE	
1. Benthamidia japonica var. *chinensis*	
EBENACEAE	
1. Diospyros morrisiana	
ELAEOCARPACEAE	
1. Elaeocarpus japonicus	*2. Elaeocarpus sylvestris* var. *sylvestris*
3. Sloanea formosana	
EUPHORBIACEAE	
1. Bischofia javanica	*2. Sapium sebiferum*
FAGACEAE	
1. Castanopsis cuspidata var. *carlesii*	*2. Castanopsis fargesii*
3. Cyclobalanopsis gilva	*4. Cyclobalanopsis glauca* var. *glauca*
5. Cyclobalanopsis longinux var. *longinux*	*6. Cyclobalanopsis morii*
7. Cyclobalanopsis pachyloma	*8. Cyclobalanopsis stenophylloides*
9. Pasania glabra	*10. Pasania hancei* var. *ternaticupula*
11. Pasania harlandii	*12. Pasania konishii*
13. Quercus spinosa	*14. Quercus tatakaensis*
15. Quercus variabilis	
FLACOURTIACEAE	
1.Idesia polycarpa	
HAMAMELIDACEAE	
1. Liquidambar formosana	
JUGLANDACEAE	
1. Engelhardia roxburghiana	*2. Juglans cathayensis*
3. Platycarya strobilacea	

(Continued)

LAURACEAE	
1. Cinnamomum camphora	*2. Cinnamomum insulari-montanum*
3. Cinnamomum osmophloeum	*4. Lindera erythrocarpa*
5. Lindera megaphylla	*6. Litsea cubeba*
7. Litsea hypophaea	*8. Machilus japonica* var. *japonica*
9. Machilus japonica var. *kusanoi*	*10. Machilus philippinensis*
11. Machilus thunbergii	*12. Machilus zuihoensis* var. *mushaensis*
13. Machilus zuihoensis var. *zuihoensis*	*14. Neolitsea acuminatissima*
15. Neolitsea konishii	*16. Neolitsea sericea* var. *sericea*
17. Phoebe formosana	*18. Sassafras randaiense*
LEGUMINOSAE	
1. Acacia confusa	*2. Adenanthera microsperma*
3. Gleditsia rolfei	*4. Maackia taiwanensis*
5. Ormosia formosana	*6. Pongamia pinnata*
MAGNOLIACEAE	
1. Michelia compressa	
MELIACEAE	
1. Melia azedarach	
MORACEAE	
1. Broussonetia papyrifera	
MYRICACEAE	
1. Myrica rubra	
NYSSACEAE	
1. Camptotheca acuminata	
OLEACEAE	
1. Chionanthus retusus	*2. Fraxinus griffithii*
3. Fraxinus insularis	*4. Ligustrum sinense*
5. Osmanthus fragrans	
PALMAE(AREACACEAE)	
1. Phoenix hanceana	
PITTOSPORACEAE	
1. Pittosporum illicioides var. *illicioides*	
PROTEACEAE	
1. Helicia formosana	
RHAMNACEAE	
1. Rhamnus nakaharae	

(Continued)

ROSACEAE	
1. Eriobotrya deflexa	*2. Malus doumeri*
3. Photinia niitakayamensis	*4. Photinia serratifolia* var. *serratifolia*
5. Prunus buergeriana	*6. Prunus campanulata*
7. Prunus matuurai	*8. Prunus phaeosticta*
9. Prunus taiwaniana	*10. Prunus transarisanensis*
11. Pyracantha koidzumii	*12. Rhaphiolepis indica*
13. Sorbus randaiensis	
RUBIACEAE	
1. Tricalysia dubia	
RUTACEAE	
1. Phellodendron amurense var. *wilsonii*	*2. Tetradium glabrifolium*
3. Zanthoxylum ailanthoides	
SAPINDACEAE	
1. Dodonaea viscosa	*2. Koelreuteria henryi*
3. Sapindus mukorossi	
SCROPHULARIACEAE	
1. Paulownia kawakamii	*2. Paulownia ×taiwaniana*
SIMAROUBACEAE	
1.Ailanthus altissima var.*tanakai*	
STAPHYLEACEAE	
1. Euscaphis japonica	*2. Turpinia formosana*
STERCULIACEAE	
1.Reevesia formosana	
STYRACACEAE	
1. Alniphyllum pterospermum	*2. Styrax formosana* var. *formosana*
3. Styrax suberifolia	
SYMPLOCACEAE	
1. Symplocos stellaris	
THEACEAE	
1. Adinandra formosana var. *formosana*	*2. Cleyera japonica* var. *morii*
3. Eurya chinensis	*4. Eurya glaberrima*
5. Gordonia axillaris	*6. Schima superba* var. *kankaensis*
7. Schima superba var. *superba*	*8. Ternstroemia gymnanthera*
TROCHODENDRACEAE	
1. Trochodendron aralioides	

(Continued)

ULMACEAE	
1. Aphananthe aspera	*2. Celtis formosana*
3. Celtis sinensis	*4. Trema orientalis*
5. Ulmus parvifolia	*6. Zelkova serrata*
VERBENACEAE	
1. Clerodendrum trichotomum	*2. Premna microphylla*

The species of seed and clonal orchards are summarized as follows: *Calocedrus macrolepis* var. *formosana*, *Chamaecyparis formosensis*, *Cha. obtusa*, *Taiwania cryptomerioides*, *Cunninghamia konishii*, *Pinus taiwanensis*, *Michelia compressa*, *Cinnamomum osmophloeum*, and *Cinnamomum kanehirae*.

Tree seeds can be divided into three classes based on storage behavior: orthodox, recalcitrant, and intermediate types in Taiwan. Orthodox seeds are tolerant to desiccation, and they can be dried to moisture contents of 5%~6% and stored at –20 °C for more than 10 years. Examples of orthodox type of seeds are *Ca. macrolepis* var. *formosana*, *Cha. formosensis*, *Cha. obtusa*, *Taiwania cryptomerioides*, Leguminosae, Oleaceae, *Phellodendron amurense* var. *wilsonii*, *Schima superba*, *Koelreuteria henryi*, *Sapindus mukorossi*, *Liquidambar formosana*, etc. Recalcitrant seeds are sensitive to desiccation, and they cannot be dried and stored at any temperature, but can be stored with moist sphagnum at 4 °C for 1~3 years depending on the species. For example, seeds of most species in the Lauraceae, Fagaceae, and Podocarpaceae, including *Diospyros* spp., exhibit recalcitrant storage behavior. Intermediate seeds are between orthodox and recalcitrant types, and they can be safely dried to about 5%~12% moisture contents and stored at temperatures above zero (4°C) for a short period of 1~3 years. However, storage of intermediate type of seeds at subzero temperatures may reduce seed germinability and longevity. For example, seeds of *Cinnamomum camphora*, *Neolitsea aciculata* var. *variabillima, Schefflera octophylla*, *Trema cannabina*, and *Zelkova serrata* are categorized as having intermediate storage behavior.

Dormancy of tree seeds can be divided into four classes: physical dormancy, morphological dormancy, physiological dormancy, and morphophysiological dormancy. Tree seeds require scarification to break dormancy in species with physical dormancy such that *Acacia confusa* seeds require treatment at 100°C to break dormancy and increase germination rates. Other examples such that *Cinnamomum camphora* seeds need treatment with 15% H_2O_2 and *Sapindus mukorossi* seeds require treatment with concentrated H_2SO_4 to

facilitate germination rates. Most dormant tree seeds exhibit physiological dormancy and require cold stratification to break the dormancy. Some tree seeds exhibit morphophysiological dormancy and require warm and cold stratification to break seed dormancy.

Management, exchange, and conservation of animal genetic resources (AnGRs)

Conservation and utilization of AnGRs

Livestock and poultry in Taiwan include pigs, cattle, water buffalo, goats, horses, rabbits, chickens, ducks, geese, and turkeys (Figure 1). Other major poultry raised by local farmers include quails and ostriches. Due to high land prices and rising environmental awareness, most local farmers operate on a small scale in rural areas of central and southern Taiwan. Coupled with import-dependent feeds and expensive labor, the local livestock industry operates with rather high production costs. Fortunately, local livestock farmers are highly diligent, and have advanced feeding and breeding skills.

Figure 1. Farm animal genetic resources in Taiwan.

The existence of threats to AnGRs in developed countries due to globalization is generally accepted, and AnGR conservation is likely to be consistently undervalued. Native breeds generally maintain one or more adaptive characteristics to the living environment, which may provide useful or potentially useful genes or combinations of genes for future needs. Examples of useful genetic traits are prolificacy and early maturity of pigs, heat tolerance of Taiwan yellow cattle, disease-resistance of Formosan buffalo, roughage tolerance of native geese, and the meat flavor of native chickens. Furthermore, most native breeds of animals in Taiwan are still raised in grazing production systems. This was recognized at the 8th Board Meeting of the Advisors for Science and Technology – Agriculture Group in April 1986, which formally recommended that life resources be preserved so that their genes will not be forever lost due to concentration on limited and highly selected strains. Consequently a large-scale pilot national project, “Germplasm Preservation and Utilization in Domestic Animals”, was initiated in 1987. There are three methods for preserving livestock germplasm: maintaining live populations, cryopreserving germ cells, and establishing DNA stores. Animal resources are bounteous and are preserved for improving exotic breeds in terms of future production performance and efficiency. Conservation and integration of germplasm for new variants were attempts to adequately use the gene pool in Taiwan from 1987 to 1992. Protocols on conserving livestock germplasm are as follows:

1. Establishment of standards for visible characteristics of conserved breeds;
2. Collection of native animals from small farms;
3. Selection of places for conservation;
4. Propagation using a small population at random; if animals have economic traits for improving production performance of exotic breeds, then intercrossing programs are implemented;
5. Phenotypic measurements and data collection on animal growth, reproduction, living habits, and genetic polymorphism;
6. Preservation of germ cells with emphasis on semen and embryo cryopreservation;
7. Information exchange of utilization and provision for public needs;
8. Typical animals after propagation with benefits of cooperative germplasm research being released to the private sector;
9. Promotion of public extension and education with intellectual property rights for this germplasm relative to arts and culture; and
10. Sharing the world’s genetic diversity resources and turning potential into reality.

Capacity building in AnGR management

Understanding the diversity and status of AnGRs provides the basis for raising public awareness. However, raising awareness without ensuring capacities to realize actions will not produce the effective management and sustainable utilization of local breeds. Animal conservation activities were further posted on the web site of ANGRIN (*www.angrin.tlri.gov.tw*) for documentation of pictures and videos of conserved and selective breeding animals from 1993 to 1998 in the second phase of animal conservation project. The importance of the conservation and sustainable use of AnGRs was recognized by policy makers and major stakeholders in the livestock sector. Strengthening the breeding capacity and programs for local breeds were established and stimulated *in situ* conservation. On the other hand, *ex situ* conservation in cell/tissue banks requires appropriate infrastructure and organization, technical capacity, legal arrangements, and sustained funding. The Taiwan Animal Germplasm Center (TAGC) is a new capacity building for managing AnGRs via cell/tissue banks with liquid nitrogen, and it serves as a conservation center under the third phase (1999~2004) of the animal conservation project.

Research and utilization of molecular techniques to verify AnGRs are understood to encompass animal genetic resources that are or have been maintained to contribute to animal protein supplies and farmer livelihoods in the fourth phase (2005~2008) of the animal conservation project. Comprehensive assessments of genetic diversity of local breeds using molecular genetic markers are required. Genetic variations within livestock species are partly attributed to differences between breeds and partly to differences among individuals within breeds. A breed or population becoming extinct means the loss of its unique adaptive attributes. The potential of new and emerging technologies, such as DNA libraries of local breeds (Table 4), is being applied to reveal the genetic bases of disease resistance, adaptation to environmental stresses, and production efficiency. Molecular methods will provide new tools for conventional and trans-formative genetic improvements.

Domestic animals supply 30% of total human requirements for food and agriculture, and 70% of the world's rural poor depend on livestock as a component of their livelihoods. As an example, there have been tremendous movements of livestock germplasm from the northern hemisphere to Taiwan driven by global production systems as compared to that from the southern hemisphere to Taiwan. Exchanges of genetic materials among regions have been a very valuable mechanism for breeding and livestock development. Taiwan farm

animals such as dairy cattle, pigs, and layers, preserve a high percentage of exotic blood through long-term agriculture trade relationships.

Table 4. Establishment of DNA libraries for farm animals in Taiwan

Species	Breed/Line	Phage	Cosmid	Fosmid	BAC
Pigs	Taoyuan		1M1F		1M1F
	Lanyu		1M1F		
	Landrace		1M1F		
Cattle	Dairy Holstein			1F	
Goats	Formosan goat		1F		
Chickens	Native inbred line 9		1M1F		1M1F
	Native inbred line 11		1M1F		
Ducks	Brown Tsaiya	1F			
Geese	Brown native			1F	
	Total	1	11	2	4

Backup system for global management

Further losses of local breeds are probably inevitable, even though local breeds are important components of our future food security and cultural heritage. Conservation of local breeds should certainly be a public concern. In the fifth phase (2009~2012) of the Taiwan animal conservation project, a global bio-identification system and exchanges of genetic resources will be carried out to develop a backup system of genetic materials and samples at the regional and global levels. Therefore, TAGC's mission consists of effective and efficient handling and documentation of AnGRs such as DNA samples, cells, and tissues generated from various germplasms in AnGR conservation, cryobanking, bioutilization, and management as follows:

1. To provide a venue to discuss the status of documentation activities of the various cryobanks of animal and forage plant genetic resources in the Asian and Pacific region;
2. To familiarize participants with various documentation systems available, germplasm documentation, data analysis, and information management for AnGRs;
3. To reinforce the capabilities of participants for conservation banking techniques, cell freezing methods, data processing, genetic analysis, and interpretation of results;

4. To provide a venue to discuss and clarify issues concerning international, regional, and national laws and policies of relevance to the conservation and management of AnGRs;
5. To increase the knowledge and understanding of participants on intellectual property rights (IPR) issues, mechanisms of access, and benefits of sharing genetic resources; and
6. To reinforce the capability of participants in dealing with said issues in relation to research and development of AnGR conservation and management.

High-output breeds or so-called international trans-boundary breeds have resulted in impressive production increases, and many countries regard them as a means of enhancing their livestock production to replace local breeds (FAO, 2007). The capacity to characterize, sustainably use, and conserve AnGRs in many countries varies due to a lack of inventory and monitoring. Moreover, inventories of AnGRs are the basis for planning development programs of local breeds. Collaboration in breeding activities between countries with similar production conditions is an opportunity to share costs and make breeding programs more sustainable. Animal health is the most regulated aspect of livestock management on a global scale. Hence, effective disease control is essential, and trade potentially presents challenges for AnGR risk management and backup systems.

In order to facilitate the collection, conservation, utilization, exchange, rehabilitation, and research of farm animal and forage genetic resources, as well as to solidify the operations and management of farm animal and forage genetic resources, the *Operation Guidelines* (document no. 0962300511 of the Council of Agriculture (COA) on January 19, 2007) were set up by the Taiwan Livestock Research Institute (TLRI). Genetic materials collected and conserved by the TLRI belong to the government, while the original provider retains the preferential right to take back part of the conserved genetic material. Under this condition, the original provider retains the preferential right to take back all of the conserved genetic materials stored at national backup inventories for risk management. When the utilization of biological materials involves IPR, the operation shall proceed in accordance with ‘’the regulation for the belongings and utilization method of scientific research and development achievements,’’ promulgated by the COA. Therefore, genetic materials of fish and other aquaculture and fisheries species, and wild relatives of livestock are kept in the cryobanking capacity of the TAGC for risk management of valuable samples. This backup concept for global genetic resource management should take the same approach among

countries and regions. A global program should be formulated to provide the institutional capacities and resources needed for its implementation at the regional level and to accept the global responsibility.

Aquatic genetic resourcebank (AGRB) at the freshwater aquaculture research center (FARC)

Tilapia fish have been cultured for nearly 60 years in Taiwan since the introduction of Mozambique tilapia (*Oreochromis mossambicus*) in 1946. At present, seven species of tilapia have been introduced and are being conserved in Taiwan. Successful hybridization and efficient selective breeding have resulted in significant development of fast-growing strains and all-male fry. These achievements have promoted the rapid development of the tilapia industry in Taiwan. In 2007, the annual production of tilapia reached 76,000 metric tons (mt), which ranked first among the top ten aquaculture species in Taiwan (Table 5). Tilapia has become the most important exotic fish species cultured in Taiwan.

Due to environment pollution, degradation of natural habitats, invasion of exotic species, and inbreeding depression of aquaculture species, the establishment of aquatic genetic resources bank is urgently needed. The objective of this genetic bank would be to facilitate the implementation of selective breeding and broodstock conservation for both economically cultured species and native fish species in rivers. Broodstock management and species identification, hybridization and its commercial application, and breeding achievements in recent years are summarized.

Table 5. Production, value, and acreage of main aquaculture species in Taiwan (2007)

Species	Metric tons ($\times 10^2$)	Value (10^6 TWD)	Area (ha)
Tilapia	761	2656	6964
Milkfish	532	2462	8865
Eel	248	7613	2006
Hard clams	357	1597	6892
Oysters	282	3215	11798
Groupers	172	3884	1554
Freshwater clams	145	592	1015
White shrimp	101	1814	2289
Giant freshwater prawn	83	3129	1948
Carp	73	357	2072

Establishment of an aquatic genebank

In order to preserve genetic diversity, secure natural resources, and improve genetic breeding of aquatic fish, the FARC was designated as the base for an aquatic genetic resource bank in 1998. After national considerations on the details of the proposal, the design of this institute was completed in 2003; construction began in 2004 and was completed in November 2005. The main facilities include a genetic conservation building, breeding and genetic building, and conservation greenhouses. The breeding and genetic building is utilized as a site for breeding and genetic conservation of tilapia. The facilities of the genebank include different-sized broodstock ponds and water recirculation systems. In addition, the conservation greenhouse is the site for preserving tilapia seedlings. The building is equipped with electric windows and fans to adjust the room temperature.

Tilapia stocks at the FARC

Oreochromis mossambicus was first introduced to Taiwan from Singapore in 1946. A low tolerance to cold temperatures and small size are two major disadvantages in fish farming. *Tilapia zillii* was later introduced from South Africa in 1963. This species did not receive much acceptance due to poor taste and slow growth. *Oreochromis niloticus* was introduced from Japan in 1966 for the purpose of genetic enhancement. In addition, for the sake of obtaining monosex progeny, *O. aureus* was introduced from Israel in 1974. Since then, two species have been added to the list of tilapia in Taiwan, *Tilapia rendalli* from Costa Rica and *O. hornorum* from South Africa, again for the purpose of genetic improvement. Additionally, the introduction of *O. spirulus* in 1991 from Saudi Arabia was due to its eurythaline features. Tilapia species stocked at the FARC are shown in Table 6.

Management of fish stocks and species identification

Because the retarded growth of cultured tilapia was largely due to poor broodstock management, resulting in inbreeding depression, much attention had to be paid to broodstock management.

Table 6. Tilapia species stocked at the FARC

Species	Year introduced	Source
Oreochromis mossambicus	1946	Singapore
O. mossambicus	1981	South Africa
Tilapia zillii	1963	South Africa
O. niloticus	1966	Japan
O. aureus	1974	Israel
O. hornorum	1981	Costa Rica
T. rendalli	1981	South Africa
O. spilurus	1981	Saudi Arabia

Generally, both broodstock and offspring are kept in ponds for two to three generations. Mass selection was adopted to carry out selective breeding. During the spawning season (from April to May), fish with superior qualities are selected to serve as spawners and are stocked in a pond for natural reproduction. Before overwintering, larvae with a large size, fast growth rate, and high conditioning factor are captured and serve as genetically superior seedlings. These fish are conserved for future use.

As for the genetically effective population (Ne), the following formula is used:

$$Ne = (4 \times N♂ \times N♀) / (N♂ + N♀).$$

If, ♂ : ♀=1 : 1,

then, Ne = 2Np.

Usually, the inbreeding rate (IR) = 1／(2Ne).

If the IR maintains below 0.25%, Ne should not be < 100 pairs for each conserved species, which is required to maintain healthy genetic variability.

Methods developed to use for species (strain) identification are listed as follows:

a. Data collection and assessment of digital pictures;
b. Data establishment of morphometric and meristic characters;
c. Analysis of chromosome – set distribution (or karyological analysis);
d. Allozyme electrophoresis – using serum esterase, hemoglobin, transferrins, and serum protein;
e. Mitochondrial DNA (mt-DNA) – polymerase chain reaction (PCR) and restriction fragment length polymorphism (RFLP) analysis; and
f. Genomic DNA – random amplified polymorphic DNA (RAPD) techniques.

Hybridization and utilization of fish stocks

Increases in production will have to come from the use of genetically improved strains. Consequently, applications of selective breeding and hybridization have been responsible for increased production efficiencies and improved productivity.

Tilapia mature at as early as 4 months old and spawn multiple times. In addition, male tilapia grows about 1.5~2-fold faster than females. Therefore, it is a common practice to culture all-male tilapia. There are two important factors which contributed to the success of commercial tilapia culture: strains with faster growth rates and larger size and production of all-male fry.

Hybridization between female *O*. *mossambica* and male *O*. *niloticus* was achieved in 1969. The hybrids have the genetic merits of a faster growth rate and larger size. This hybrid strain resulted in the rapid development of tilapia culture in Taiwan. Hybrids between female *O. niloticus* and male *O. aureus* were obtained which produced a high percent of male progeny in 1975. The culture of all-male fry successfully brought the tilapia industry into commercial-scale production in Taiwan.

Hybrids derived from *O. niloticus* and a mutant of *O. mossambicus* by interbreeding were obtained and have been maintained since 1968. After successive selective breeding, a pure-red color strain was recently produced with only a few spots, and in some cases, not even a single spot (Figure 2).

Currently, *O. niloticus* is the target species for experiments of selective breeding. To the present, four conserved strains have been selected and exhibit good growth performance. In view of the fact that some of the strains hybridized with *O. aureus* could produce 100% all-male progeny, tilapia species are being conserved in the genetic resource bank of the Center.

A faster-growing strain of tilapia was developed in 2006 through hybridization of *O. niloticus* and *O. aureus.* This strain showed a 30% higher body weight on average compared to locally farmed strains.

Digestion of the D-loop region, using *Acu*I, *Bbs*I, and *Msp*I restriction enzymes, resulted in several different restriction patterns. This PCR-RFLP technique was developed in 2007 to discriminate five tilapia species conserved at the FARC.

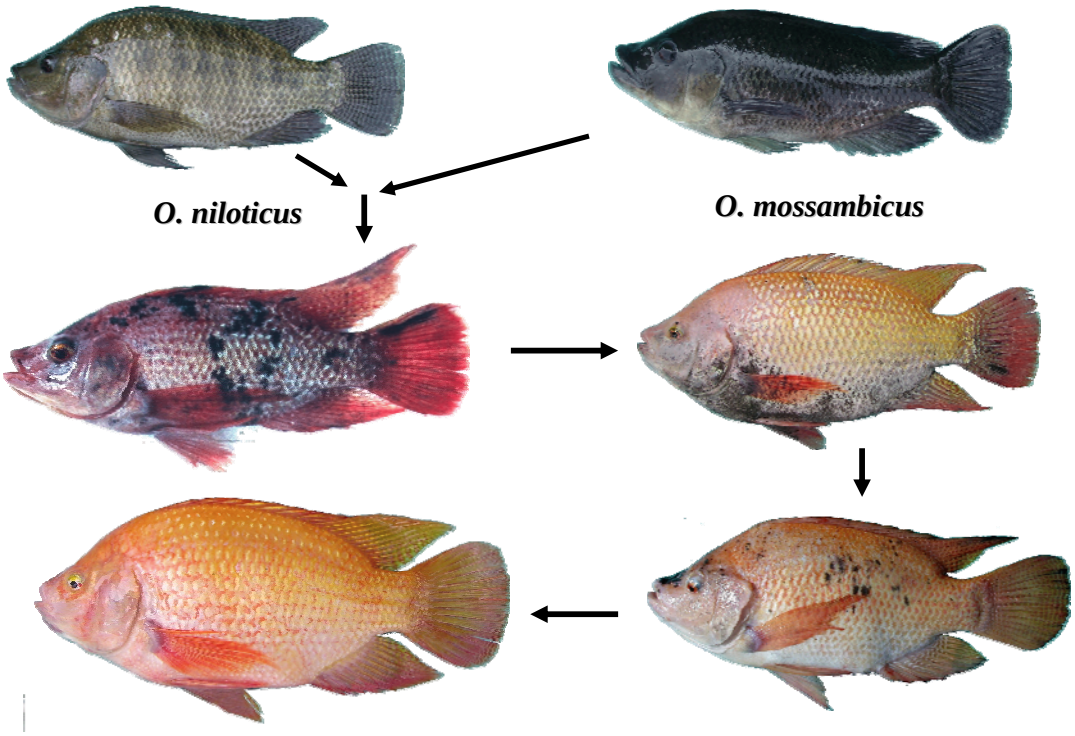

Figure 2. The pure-red strain of tilapia derived from interbreeding of *Oreochromis niloticus* and a mutant of *O. mossambicus*.

The coloration of red tilapia varies with size and environmental conditions. In addition, black spots also appear in the late period of culturing. There seems to be a tendency for its genetic expression mainly from a recessive gene. The experiment of selective breeding accordingly focused on increasing homozygous mating.

After long-term crossbreeding, the effects of inbreeding depression are likely to occur due to genetic bottlenecks resulting from very few fish having been imported originally. Since importation is very difficult to achieve, devising a good approach to prevent this negative effect is, therefore, the first priority. From the viewpoint of genetic variance, wild stocks are more important than cultivated ones. In this aspect, there is an eager requirement to introduce wild stocks from foreign countries.

Risk management of agricultural genetic resources

Risk management

The objectives of risk management are first to recognize the duty, mission, and policy implementation of the institute, determine the risks that can effect the objectives of policy implementation of the institute, and appreciate the internal and external environments for policy implementation when it is to make decisions. Then, these events will be researched and analyzed, and the extent of the impacts of actions can effectively be managed to lower risks, and the probability can be minimized even in a crisis. Therefore, when events occur, theirs impacts can still be minimized.

The government began to facilitate implementation of risk management for institutes and organizations in 2005, and it has sponsored risk management for executive and professional study classes, compiling operation manuals of risk management, and establishment of a risk management knowledge network and an expert counseling hotline to promote the beliefs in risk management as well as to advocate the fundamental concepts of risk management for integration with domestic and overseas knowledge and experiences. Furthermore, it has also introduced measures of implementation in the public sector to conduct an integrated cooperative framework and practical operations of risk management. In addition, the government has included “risk management” in the program content of management study camps of public servants to enhance their capability building.

Risk mitigation

Natural risk mitigation strategies can reduce the impacts concentrated on our nation’s genetic resources, large employment, public infrastructure, and critical facilities. Natural risk mitigation for genebanks may include developing emergency management services and training employees’ capability to deal with a contingency before an event occurs, and establish mitigation strategies. Collaboration among the public and private sectors to create mitigation plans and actions can reduce impacts of natural hazards. In developed countries such as Canada, the UK, and Australia, their government departments have, for years, introduced risk management, while we have merely just begun to consider risk management. Therefore, the concepts of integrated risk management of every institute remain at the initial stage. Capacity building of risk management for institutes desperately needs greater inputs and efforts. We believe that losses resulting from risks can be reduced, and more success can be achieved through effective implementation of risk management.

Capacity building

Seed genebanks are established to maintain the viability and life-span of plant seeds in the long term. As a result, banks should be equipped with facilities to maintain low temperatures and low humidities as well as to endure natural environmental changes and man-made disasters. Furthermore, they should also be staffed with professional personnel and have the financial resources to maintain regular operation of relevant management systems.

In the world of nature, there may be disasters that can generate relatively large-scale risks to seed banks; 1. abiotic disasters such as earthquakes, flooding, fires, landsides, lightning strikes, and flying objects, which may result in the collapse and destruction of seed banks; and 2. biological disasters including the destruction and poaching by microorganisms, insects, birds, mice, animals, and human beings.

To strengthen the buildings and facilities, seed genebanks are constructed to withstand earthquakes, floods, typhoons, and other natural disasters. In addition, the structure of the building can withstand an earthquake of up to magnitude 7 on the Richter scale (while regular buildings can withstand a magnitude 5 quake), and the building is of a stabilized square-structure with a raft foundation so that the entire building vibrates with the quake to reduce damage. As for fire-fighting equipment, most office buildings make use of fume-detection sprinkler systems, while mechanical warehouses with lubricant oil heat-detection and self-solid systems of fire fighting equipment will be installed. In the seed bank, the computer room and seed bank have fume-detection and heat-detection inertial gas fire-prevention systems to prevent equipment and plant species from being destroyed by fire-detection sprinklers in the seed bank. In front of the building, there is a pool for fire-fighting vehicles during a fire. Furthermore, the seed bank building is designed so that the core of the building can withstand a collision with a flying object, and it is then surrounded by various other buildings.

In most developing countries, capacity building for managing seed genebanks and field genebanks lacks long-term support for national management systems of genetic resources, which results in a lack of effective access to germplasm and relevant technologies. Other limitations have to do with insufficient trained personnel, shortcoming of facilities, and inefficiencies in administration. Raising the capacity to manage genetic resources at the international, national, and regional levels requires the training of more experts and curators/stakeholders and the development of an integrated risk management system. The

TARI has drawn mid-term specific objectives for capacity building strategies aimed at enhancing integrated management systems of national genebanks. These strategies support policy development, provide education and training, facilitate access to relevant technologies, construct back-up systems for global management, and facilitate exchange of genetic resources and sharing of information to effectively utilize genetic resources to meet producer and consumer needs and address food security and livelihood concerns.

Conclusions

The nursery industry and utilization of bioresources including plants, aquaculture, livestock, and microorganisms, are considered the most potentially competitive agriculture industries in Taiwan. In recent years, because species improvement has targeted high yields and uniformity so that the materials used tend to certain genotypes, broadening the genetic diversity to enhance the adaptability of new species is a necessary measure for resource conservation and future nurseries. These measures involve collecting native and exotic species for trait investigation and conservation, updating germplasm year by year to ensure the genetic security of strains/stocks/varieties so as to maintain and utilize the genetic resources for food and agriculture.

Biodiversity is the key research topic of global interests. Other than research on diversity of ecosystems, species, and genetics, using molecule technologies makes research on genetics and gene diversity more convenient and rapid. Planning measures and policy decisions of bioresource conservation must refer to more bioinformatic information on the genetics, species, and ecological diversity involved. The establishment of DNA bar codes of species and gene databases will help researchers share bioinformatics of genetic resources. To access germplasm materials for global ecological conservation and sustainable use, establishing a nation’s genebanks and preservation of germplasm are effective ways to efficiently utilize natural resources, and overcome global climate changes while simultaneously improving food and agricultural production.

Biological diversity is a natural resource. All nations share the responsibility for its management and the privilege of using it. Individuals, the private sector, and other groups can contribute to the maintenance of germplasm, but the tasks of overseeing and managing genetic resources are clearly beyond the capacity of any individual or group. Coordination of the many varied efforts including international collaboration must occur through fully supported and funded national programs.

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Conservation and Risk Management of Plant Genetic Resources in Thailand

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Abstract

There are many relevant organizations that are active in the conservation of plant genetic resources in Thailand, namely organizations which are under the responsibility of the Ministry of Agriculture and Cooperatives, organizations which are under the responsibility the Ministry of Natural Resources and Environment, and also some academic institutions. The Department of Agriculture has played significant roles as a key national organization which is responsible for agricultural genetic resource conservation, whereas the Royal Forest Department is accountable for forest genetic resource conservation. Examples of universities which are carrying out conservation of plant genetic resources are Chiang Mai University, Khon Kaen University, Maejo University, and Prince of Songkla University. To maintain good management of plant genetic resource conservation, it is necessary for all sectors to analyze and handle the potential risks which both directly and indirectly affect conservation.

This report describes potential risks to plant genetic resource conservation: 1) difficulties of management that are the result of changing policies, insufficient budgets, and retirement of genebank experts; 2) the loss of plant genetic resources that are the result of natural disasters, biotic and abiotic stresses, genetic erosion, and lack of awareness of genetic resource values; and 3) regeneration of mixed genotypes in the same accession which can lead to the loss of minority ones. In order to minimize these risks, some management practices should be carried out; for instance, duplicate collection of both on-farm conservation and genebanks can save genetic resources from unexpected incidents like natural disasters. Some systems should be created to prevent the consequences of changing policies on plant genetic resource conservation. Moreover, building public awareness of the value of genetic resources should be done by promoting their utilization.

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Finally, human resource development is urgently needed. The staff should attend training sessions and workshops to enhance their expertise and knowledge. Like other countries, Thailand tries to manage and minimize the risks with all its capability even though some factors are out of our direct control.

Introduction to Thailand

General Basic information

The Kingdom of Thailand is situated on the Indo-China Peninsula, covering an area of 514,000 square kilometers. It shares borders with the Union of Myanmar to the west and north, Lao P.D.R. to the north and northeast, the Kingdom of Cambodia to the east, and Malaysia to the south. It is divided into four distinct areas: the mountainous north, the fertile Central Plains, the semi-arid plateau of the northeast, and the peninsular south, distinguished by its many beautiful tropical beaches and offshore islands. Thailand lies within the humid tropics. There are three seasons: the cool season (November to February), hot season (April to May), and the rainy season (June to October), although downpours rarely last more than a couple of hours. The population is about 60 million. Ethnic Thais form the majority, although the area has historically been a migratory crossroads, and thus strains of Mon, Khmer, Burmese, Lao, Malay, Indian, and, most strongly, Chinese blood produce a degree of ethnic diversity. Integration has, however, produced enormous unity both culturally and socially.

Agricultural Sector Information

Thailand is a small country of approximately 320,700,000 rai (2.5 rai = 1 acre). The agricultural sector is classified into four major groups of livestock, fishery, vegetation, and forestry. According to the Office of Agricultural Economics, the total area of Thailand is divided into many categories depending on the usage: forests (104,744,313 rai), agricultural land (130,275,993 rai), and wastelands or grasslands (2,532,003 rai).

Almost all of the agricultural land is used for growing rice (63,861,066 rai), field crops (27,400,423 rai), horticultural crops (29,017,779 rai), and livestock (1103.3 rai). The agricultural sector dominates the Thai economy, providing two-thirds of employment and almost half of total exports. The economic crops are rice, para rubber, maize, sugarcane, sorghum, cotton, soybeans, pineapple, oil palm, ornamental flowering plants, etc. Not only do these crops bring great national profit to the country, they also enhance farmers' earnings in terms of household income.

The vegetation is divided into two major zones, namely lower tropical rainforests and upper tropical rainforests. Lower tropical rainforests occupy the peneplains and also hill slopes up to 600 m in elevation, whereas upper tropical rainforests cover slopes of 600 to 900 m. To produce good varieties and good seeds, germplasm may be obtained by collecting from the wild, landraces, and cultivated areas, and has been introduced from foreign countries. Today there is more progress in the production of good seeds. Cooperation between the government and private sector is underway particularly in the use of modern technologies. However, seeds produced by the government are limited in quantity, so seed supplies rely on those stored by farmers themselves or produced locally.

Status of plant genetic resource conservation in Thailand

Relevant organizations

In fact, there are many organizations which conduct plant genetic resource conservation throughout Thailand. The outstanding organizations can be briefly described as follows:

1. Department of Agricultural Extension

The Department of Agricultural Extension is also under the jurisdiction of the Ministry of Agriculture and Cooperatives. It plays a role as a key organization which engages in extension and distribution of good varieties. There are regional offices which are located in almost every district of the country. Its distinguished missions regarding plant genetic resource conservation are good varieties of horticultural crop collection for the purpose of propagation and distribution to farmers. In total, 46 species of crops have been collected, such as mango, longan, lychee, jackfruit, pomelo, durian, mangosteen, orange, macadamia, pomegranate, rose apple, etc.

2. Universities and academic institutes

Almost every institution has collected and conserved plant genetic resources in both the field and laboratory. The collections are kept in accordance with their objectives of research and study programs. Some examples are as follows.

Faculty of Agriculture, Chiang Mai University carries out conservation of plant genetic resources with the objectives of collecting and conserving materials for investigations and

research including studies on suitable means of resource utilization. Plant germplasm can be grouped into cereals, legumes, herbs, native species, beverage plants, vegetables, and fruit tress. All plants are *ex situ* conserved.

The plant germplasm collection at Khon Kaen University is carried out by the Faculty of Agriculture. The Departments of Agronomy and Horticulture are responsible for this job. The collected germplasm includes sesame, peanuts, soybeans, cowpeas, yard long beans, tamarind, guava, etc.

Maejo University has been conserving plant genetic resources both *in situ* and *ex situ*: for example, the Plant Genetic Resources Conservation Project in Banpong Forest conserves 223 species of herbarium specimens, the Department of Agronomy conserves six species of agronomic plant genetic resources through field collections, a seed bank, and germplasm, the Department of Ornamental Horticulture (Vegetable Technology) has collected five species of economically important vegetables including nine varieties in a seed bank and 23 species of important local vegetables from four provinces in northern Thailand through field collections and a seed bank, and the Department of Ornamental Horticulture (Pomology) has conserved 11 varieties of longan (*Dinocarpus longan* Lour) and nine varieties of lychee (*Litchi chinensis* Sonn) through field collections.

Prince of Songkla University receives a budget from the Princess Sirindhorn Royal Project on Plant Genetic Resources Conservation to carry out the conservation of seven varieties of rattan and also local durian varieties.

3. Royal Forest Department

The main mission of the Royal Forest Department is to conserve and protect forest genetic resources. Recognizing the threat to valuable forest genetic resources, the Royal Forest Department has taken steps toward both *in situ* and *ex situ* conservation. In total, about 200 natural reserved areas have been established. Efforts to encourage an understanding of the importance of conservation projects among local populations are very important.

The Natural Resources Conservation Office is responsible for the project of forest natural resource conservation and management. It conducts *in situ* conservation called “protected areas” like national parks. Another important office is the Forest Research Office

which is responsible for *ex situ* conservation. Existing conserved flora include pine, teak, hardwood species, bamboo, Ma cha mong (*Afzelia xylocarpa* Craib), eucalyptus, etc.

4. Queen Sirikit Botanic Garden

The Queen Sirikit Botanic Garden (QBG), Maerim, Chiang Mai Province, was established in 1992 by the Botanical Gardens Organization of Thailand. It was the first true botanical garden in the country. The conservation programs include *in situ* conservation and *ex situ* conservation (field, seed banks, and *in vitro* conservation). Rare species and endangered species are emphasized. Living collections under its protection include 11 families and four groups such as Palmae, Orchidaceae, Moraceae, Musaceae, Caesalpiniaceae, ferns, and medicinal plants.

Collaborations in scientific research, information exchange, and training programs are encouraged at the QBG. Furthermore, coordination with other national and international institutions in conservation of plant genetic resources has been undertaken.

5. Department of Agriculture (DOA)

The DOA, a governmental sector under the Ministry of Agriculture and Cooperatives, has played a significant role in the collection, conservation and research of plant genetic resources. Almost all of the crops it is responsible for are economically important crops. Conservation can be divided into two types of *ex situ* and *in situ* conservation.

There are 40 regional crop research centers and stations throughout the country, which have conserved about 127,416 accessions. Most of them are horticultural crops which comprise 5334 varieties of fruit crops (e.g., durian, mangoes, rambutan, pineapples, and bananas), 1430 varieties of vegetables (e.g., baby corn, garlic, chili, and onions), 1109 varieties of ornamental plants (e.g., orchids, roses, and lilies), 698 varieties of industrial crops (coconut, oil palm, para rubber, coffee, and cocoa), and medicinal plants. Besides horticultural crops, other field crops are also conserved include 594 varieties of cassava, 453 varieties of sugarcane, paper mulberry, five varieties of kapok, 30 varieties of jatropha, and 36 varieties of ramie.

As to seed banks, plant genetic resource conservation particularly for rice was conducted after the end of World War II. In the early period, those conserved crop seeds were kept in air conditioned rooms. Consequently, seed longevity was quite short and caused

problems of regeneration for maintaining the varieties. In 1981, the DOA received donated money from the Government of Japan to set up the first seed bank located at the Pathumthani Rice Research Center. It is called The National Rice Seed Storage Laboratory for Genetic Resources. Not only are rice seeds conserved, other crops from many sources are also kept there. Until 2002, according to reorganization, collections from the first seed bank were transferred to a new location in the Sirindhorn Plant Genetic Resources Building, Biotechnology Research and Development Office. The main responsibilities are collection, conservation, and utilization of plant genetic resources.

Storage facilities in DOA's seed bank

- **Incoming seed room**: The room is 40 m^2 and maintained at 15 °C and 60% relative humidity (RH). Before being stored, seeds are placed in this room to determine moisture content and germination tests as well as to reduce the moisture content. Seeds ready for seed bank storage must be at an 8% moisture content and possess 80% germination.
- **Laboratory room**: This room has two parts: a) a space for a hot air oven and seed germinator, and b) space for moisture and germination analyses and purity tests.
- **Unheated seed room**: This room is used for seed moisture reduction with its low level of RH of 6%.
- **Sun drying room**: This room is used for moisture reduction using the sun's heat. When the room temperature reaches 43 °C, a heater is automatically switched on to increase the temperature. A computer is used to control the system.
- **Medium-term storage**: Its capacity is about 150,000 accessions. The room temperature is maintained at 5 °C with 60% RH. An automatic bullet crane system controlled by a computer is used.
- **Long-term storage**: This room is 86 m^2 in size and its temperature is maintained at –10 °C. Seeds are packed in vacuum-sealed aluminum foil packages. The maximum capacity is 40,000 accessions.
- **Information processing room:** Information is recorded on both computers and in documents in this room. Information records are passport data, characteristics and evaluation, percent seed germination, weight of stored seeds, rejuvenation data, seed distribution data, etc.

Status of the collections

Collections consist of both active and base collections that are maintained in PET plastic bottles with silica gel inside at 5 °C storage in vacuum-sealed aluminum foil packages at -10 °C storage conditions (Table 1).

Table 1. The total number of 30,029 accessions stored in genebanks in Thailand.

No.	Crops	No. of accessions
1	Rice	24,535
	Native and improved varieties	20,899
	Overseas varieties	2571
	Wild species	1065
2	Cowpeas	83
3	Sesame	241
4	Corn	113
5	Black gram	446
6	Safflower	72
7	Cotton	330
8	Soybeans	1923
9	Jute	50
10	Peanuts	1840
11	Vegetables	22
12	Others	374
Total		30,029

Rice is the majority whereas other plants are also conserved including cowpeas, sesame, corn, black gram, safflower, cotton, soybeans, jute, peanuts, pigeon peas, roselle, castor beans, kenaf, wheat, barley, and several varieties of vegetables.

Moreover, there are duplicate collections of rice collections at the International Rice Research Institute (IRRI).

Total accessions		5,981
	1. *Oryza sativa*	5,492
	2. Wild species	489

Regeneration and utilization

Regeneration is usually carried out on accessions when they approach the low percentage of germination (< 50%) and weigh < 50 g. Actually, regeneration must be done in order to enhance the quality and quantity of existing collections.

As regeneration is carried out; the use of the collection continually proceeds. Main users of materials in the seed bank are researchers (from both governmental and private sectors), plant breeders, students, farmers, and other users with various requirements. Many collections have frequently been used as materials for different objectives, e.g., research, breeding programs, and academic purposes. Presently, rice is the only plant which can be given upon request. Each accession can be provided if it has a high percent of germination and adequate amounts. Other crops will, hopefully, be distributed to recipients in the near future.

Laws and relevant legislation

Thailand signed the Convention on Biological Diversity (CBD) on 12 June 1992 and became a party of the CBD on the 29 January 2004. The Ministry of Natural Resources and Environment is responsible for the national focal point of the CBD and cooperation with the DOA as the competent authority of plants/crops.

Regarding intellectual property protection, Thailand has enacted several laws that are applicable to the protection of biotechnological products and processes, namely, the *Patent Act*, *Plant Variety Protection Act*, *Bill on the Law of Trade Secrets*, etc. Thai patents are given to inventions and processes which are new, posses an inventive step, and are capable of industrial application. However, patents are not given to naturally existing microorganism or their components, animals, or plant extracts. The *Thai Patent Act* is still struggling with protecting DNA, genes, and proteins, particularly those extracted, isolated, and purified from plants and animals. The issue of patentable subject matter is indeed not only a question of law but also a policy consideration.

For the International Treaty on Plant Genetic Resources for Food and Agriculture, (ITPGRFA) which Thailand signed on 4 November 2002, our country has not yet ratified it due to a government decision.

Risk management on plant genetic resources

Potentials risks and their causes

Risk 1: Difficulties in managing plant genetic resource conservation

Cause 1 – Changing policies

According to the instability of Thai politics, changing policies frequently occur within the governmental sector. For example, because of a reorganization of the Ministry of Agriculture and Cooperatives, all agricultural crops were previously under the DOA's jurisdiction, but in the last 2 years the Rice Department was set up in order to oversee all activities concerning rice. The DOA itself still has to conserve rice collections whereas the Rice Department simultaneously carries out the same activities. Unavoidably, an overlap of missions occurs.

A second example which is a result of changing policies is the direct impact on on-farm conservation. Nowadays energy crops are considered to be a hot worldwide issue. Like in other countries, Thailand currently promotes expansion of areas planted in energy crops due to strategies of the government. Thus, the lands formerly dedicated to on-farm conservation are being invaded and replaced.

Cause 2 – Insufficient budgets

Adequate money is necessary for every operation. By comparison, inadequate budgets are considered important obstacles to meeting many commitments. In Thailand, there are many research projects and activities on genetic resource conservation. Unfortunately, some of them have not received enough fiscal support from the sponsor. Thus, they cannot accomplish their goals.

Cause 3 – Retirement of genebank experts

Nowadays, the numbers of experts in genebanks tend to decrease for several reasons. One obvious reason is retirement. Those vacant positions are replaced by young staff who do not have much expertise or profound knowledge. What is more, these new staff members are not enthusiastic about this work because they do not have sufficient motivation, do not receive encouragement, and so on.

Risk 2: Loss of plant genetic resources

Cause 1 – Natural disasters

Each year, Thailand frequently faces impacts of natural disasters such as flooding, wildfires, storms, and mudflows. These severely harm plant genetic resources and especially directly affect *in situ* and on-farm conservation efforts. These rapidly damage natural resources and seem to be out of control whether any measures are tried to prevent their effects or not.

Cause 2 – Biotic and abiotic stresses

For field collections, plant genetic resources can be threatened by both biotic (pathogens, insects, and other pests) and abiotic stresses (drought, flooding, global warming, and other environmental factors). These stresses lead to the loss of resources and are sometimes simultaneously beyond prevention and control.

Cause 3 – Genetic erosion

Because of advancements in plant breeding, many new improved varieties with dominant genes like those for pest resistance are likely stronger than older cultivars. So, many local varieties can potentially lose their original genetics and tend to be replaced by high-yield varieties.

Monoculture is also a major cause of genetic erosion. For instance, many farmers consider that one crop is the preferred crop. At the same time, other local crops are neglected because of their weaknesses and incompetence such as low yields and lack of pest resistance. In consequence, those local varieties tend to be supplanted and eventually lost.

Other human behaviors such as deforestation, improper use of modern technologies, and lack of sustainable use of natural resources can threaten plant genetic resources in both direct and indirect ways; for example, gathering various kinds of forest resources especially rare and endangered species can lead to their extinction.

Cause 4 – Lack of consciousness regarding evaluations of plant genetic resources

Presently, there are a lot of genetic resources the value of which has not been evaluated, because they tend to be overlooked by many farmers and researchers. Hence, their useful characteristics are not being utilized.

Risk 3: Mixture of genotypes

Most scientists have as their objective the collection of genotypes for building up genetic diversity so that there are many collections which are kept in genebanks, especially upland rice, which has mixed genotypes in the same accession. When regeneration is carried out for many generations, the stronger or predominant genotype will be in the majority because the weaker varieties are oppressed.

Risk management

Although there are several risks with plant genetic resource conservation, they can probably be managed in order to minimize the threats. We, however, should realize that the management practices we choose to handle many risks must be able to be properly implemented and must not affect other sectors.

Duplicate collections in other places should be done for both on-farm conservation and genebanks, in order to save them from unexpected incidents like natural disasters. For example, the conserved collections in genebanks should be deposited in other genebanks such as places located abroad. At present, there are approximately 5,000 accessions of rice from the DOA genebank kept at the IRRI. What's more, studying further techniques which can be other alternatives of conservation of on-farm collections such as slow growth (growth-retardant method) and cryopreservation seem necessary. These optional methods can minimize the effects of both biotic and abiotic stresses.

Some systems should be created to prevent the consequences of changing policies on plant genetic resource conservation. Moreover, the building of public awareness of the value of genetic resources for people especially local people should be done by promoting utilization, educating them about the importance of the resources, and trying to build up their consciousness that the genetic resources are national treasures so that they realize how to protect and use genetic resources in sustainable ways.

Finally, human resource development is urgently needed. With many experts in the field of genetic resources conservation retiring, young staff in each sector should be supported to enhance their knowledge and expertise. Not only do they need to attend training sessions and workshops, older staff members also need to convey knowledge from actual practice.

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Status of Conservation of Agriculture Genetic Resource in Vietnam

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Abstract

Located in tropical and subtropical areas of Southeast Asia, Vietnam has some of the most abundant agricultural biodiversity in the world. Nowadays, the agriculture genetic resource conservation system in Vietnam includes 18 key units that are implementing agriculture genetic resource (AGR) conservation with three main groups: animals, plants, and microorganisms. In addition, there are other organizations involved in this issue including veterans, women, plant breeders, and old peoples clubs, Departments of Agriculture and Rural Development, and farmers and farm-households.

AGR conservation includes five main activities in Vietnam:

- Inventory and collection of genetic materials;
- Long-term and safety maintenance of collected genetic materials (*in situ* and *ex situ*);
- Evaluation of collected genetic materials;
- Documentation of genetic materials; and
- Exchange of data information and genetic resources.

Introduction

Conservation and maintenance of animal, plant, and microorganism genetic resources comprise genetic resource conservation in order to provide initial materials for science research, improve breeding fields, and ensure the maintenance of biodiversity and essential prime materials of biological resources for sustainable development of modern and future agriculture.

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In general, genetic resources and AGRs particularly play important roles in economic and social development programs in every country. Therefore, AGR management and conservation can provide favorable conditions for sustainable agriculture development.

With great diversity and abundant plant, animal, and microorganism genetic resources, Vietnam is recognized as one of the 15 countries with the most diverse and abundant genetic resources in the world. Therefore, the Vietnamese government has been investing funds for genetic resource conservation since 1987. After more than 20 years, AGR conservation tasks have achieved some goals of specializing in collecting and maintaining genetic resources.

Documentation of AGR management in Vietnam

Conservation of AGRs is carried out by the Vietnamese government as stipulated in documents such as laws, ordinances, decrees, and decisions. The main documents include the following:

- *Law on Fisheries* dated 26 November 2003;
- *Law on Forest Protection and Development* dated 3 December 2004;
- *Ordinance on Plant Protection and Quarantin*e dated 25 July 2001;
- *Ordinance on Plant varieties* dated 24 March 2004;
- *Ordinance on Livestock breeds* dated 05 April 2004;
- Decree no. 07/CP dated 5 February 1996 by the government on the management of plant seeds;
- Decree no. 23/2006/ND-CP dated 3 March 2006 by the government on the implementation of the *Law on Forest Protection and Development*;
- Decree no. 14/CP dated 19 March 1996 by the government on the management of domestic animals;
- Decision no. 845/TTg dated 22 December 1995 by the Prime Minister ratifying the "Plan of Action to protect the biodiversity of Vietnam "; and
- Decision no. 2117/1997/QD-BKHCN&MT dated 30 December 1997 by the Minister of Science, Technology and Environment to issue the regulation on the management and preservation of plant, animal and microorganism gene sources.

The above documents set up a legal framework and favorable conditions to make genetic conservation activities into rules, and in fact, these activities have reduced the erosion of AGRs, promoted the collection and conservation of valuable genes, and concretely and realistically contributed to national programs on plant and animal breeding.

AGR conservation system in Vietnam

1. Crop production and plant protection sectors:

- The Plant Genetic Resources Center: conservation of plant genetic resources.
- Soil and fertilizer Research Institute: conservation of microorganism genetic resources in crop production.
- Plant protection Institute: conservation of genetic resources in plant protection.
- Hevea Research Institute: conservation of hevea genetic resources.

2. Forestry sector:

- Forest Science Institute: conservation of forest plant genetic resources.
- National Parks: Ba Vi (Ha Tay Province), Bach Ma (Thua Thien Hue Province), Ben En (Thanh Hoa Province), Cat Tien (Dong Nai, Binh Phuoc, and Lam Dong Provinces), Cuc Phuong (Ninh Binh, Thanh Hoa, and Hoa Binh Provinces), Tam Đao (Vinh Phuc, Thai Nguyen, and Tuyen Quang Provinces), and Yokdon (Dak Lak Province): conservation of valuable plant and animal genetic resources in national parks.
- Forestry University: conservation of endemic and valuable forest plant genetic resources.

3. Animal husbandry and animal health sectors:

- Department of Animal Health: conservation of microorganism genetic resources involved in animal health.
- Bee Research and Development Center: conservation of bee genetic resources.
- Animal Husbandry Institute: conservation of animal genetic resources.

4. Fisheries sector:

- Research Institute for Aquaculture No I: conservation of freshwater fisheries genetic resources.
- Research Institute for Aquaculture No III: conservation of brackish-water and seawater fisheries genetic resources.

Status of AGR conservation

In terms of plant genetic resources, there are 150 protein tree species, 130 fruit tree species, 100 oil tree species, 90 fiber tree species, more than 1000 wood tree species, 3850 plant species used for medicine, and several hundred cosmetic tree species.

There are more than 12,000 plant species in the forests, among which there are 7,000 species which belong to 1850 lines of 267 angiosperm families. About 2,300 forest tree species can used for food, medicine, animal feed, or materials for national economic wood purposes.

There are 275 species and subspecies of mammals, 1026 bird species and subspecies, 260 reptile species, 32 amphibian species, 500 freshwater fish species, about 2000 marine fish species, and tens of thousands of invertebrates.

Recently, conservation units have concentrated on investigating and collecting genetic resources in domestically and overseas by different methods. So, thousands of extant breeding populations were collected and genes were discovered.

1. Crop production and the plant protection sector

a. Plant genetic resources:

In general, plant genetic resource conservation tasks have been implemented including investigations, collections, maintenance, and characterization, while detection of valuable genes and use for breed selection have been limited.

- This is a key unit (The Plant Genetic Resources Center) with 19 net units. Up to 2007, they maintained about 20,000 accessions of various crops *ex situ* and *in situ*. This invaluable national property preserves valuable genetic materials.
- Nearly 150 accessions were utilized from 2001 to 2007.
- More than 15,000 accessions have been documented (morphology).

b. Microorganism genetic resources:

- In total, 664 microorganism strains belonging to 30 bacterial, fungal, Antinomyces, and yeast families are being maintained. The collected strains were preserved by traditional and modern methods (slant agar in cold conditions, below mineral oil, liquid nitrogen freezing, etc.) to maintain the characteristics of the strains.
- Software of genetic management has been set up to support data management and fast access to data.

- In total, 535 microorganism strains have been isolated, and selected from soils, roots, and medical waste samples in different areas. In total, 109 microorganism strains used for crop production were added to the collection.
- A total of 330 of 664 microorganism strains have been evaluated.
- In total, 120 microorganism strains are being used for research and utilization in agriculture production like bio-fertilizers, biological preparations for plant protection, and so on.

2. Animal husbandry and animal health sectors

- Animals: 33 breeds are investigated and inventoried; 48 breeds are conserved and maintained; 44 breeds are evaluated; 12 breeds are exploited and utilized; 58 breeds documented.
- Bees: Four breeds are investigated and inventoried, and five breeds are conserved and maintained, in which one breed is evaluated, and three breeds are exploited, and four breeds are utilized and documented.
- Animal health sector: During that time, many animal breeds have been redressed and developed, and numerous genetic materials have been conserved *ex situ*. 48 microorganism strains, including 32 bacterial strains and 16 viral strains have been conserved and maintained. All of them are periodically examined. These viruses and bacteria are supplied for vaccine control, manufacturing, teaching, and research.

3. Forestry sector

About 1800 forest organisms are being maintained and conserved *in situ* and *ex situ* on over more than 250 hectares. *Ex situ* conservation needs a large budget so that highly valuable trees are protected. About 1300 trees were exploited and utilized for growing conservation forests, and protecting forests and economic forests.

4. Fisheries sector

- Fisheries genetic resource conservation tasks were implemented in three ecosystems in Vietnam. 50 freshwater fish clones and species and ten highly valuable brackish-water and seawater fisheries species were also collected and implemented. Every year, new genes are added, while old genes are developed and exploited. These clones and species are maintained and conserved in ponds, tanks, cages, or laboratories.

- Genetic resources of 35 species were exploited and exchanged between areas of the country as well as overseas to diversify and increase abundances of cultivated fish. Recently, fisheries genetic resource conservation and maintenance have concentrated on *ex situ* methods.

International cooperation sector

International cooperation on agriculture genetic resource conservation has been implemented very well in recent times. We have established cooperative relations with several countries, international organizations, and non-governmental organizations. Some international cooperative ventures that have been implemented include the following:

- Plants: cooperation with the International Plant Genetic Resources Institute (IPGRI), International Rice Research Institute (IRRI), Asia Vegetable Research and Development Center (AVDRC-The World Vegetable Center), International Center for Tropical Agriculture (CIAT), FAO, etc.
- Animals: cooperation with the FAO, Japan, Holland, etc.
- Microorganisms: cooperation with Australia, Laos, the FAO, etc.

Constraints on agriculture genetic resource conservation tasks

- Budgets are limited so investment in building and improving genetic conservation units, buying equipment, and training human resources has not yet been satisfactory for diversifying and increasing agriculture genetic resource conservation in Vietnam.
- AGR conservation tasks have just concentrated on investigation, collecting, maintaining, and initial evaluations. Detailed evaluation and exploitation, and utilization have been limited.
- Organization networks are insufficient and incomplete, and have overlapping tasks. Germplasm identifying priorities is also recommended.

Action directions of AGR conservation in the future

- Promoting evaluation and exploitation of AGRs that are maintained in genebanks and network units;
- Promoting investigations and inventories to supply, restore, and conserve valuable plant and animal breeds;
- Propagating information on necessary AGR conservation for everyone to understand that genetic resource conservation is related to sustainable agriculture development, food safety, and environment protection; and
- Developing international cooperation for exchange experience to approach and share genetic resource benefits.

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APEC-ATCWG Workshop (2008)
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Summary Report

The APEC-ATCWG workshop entitled “Capacity Building for Development and Implementation of Risk Management Systems on Genetic Resources (GRs) for Food and Agriculture” was held in Taichung, Taiwan on 14-17 October 2008. The workshop was funded by the Council of agriculture (COA) and was hosted by Taiwan Agricultural Research Institute (TARI). In total 32 participants attended the workshop, including representatives from 12 member economies. The program and participants are provided in Appendices 1 and 2.

This workshop was to provide academic, knowledgeable presentations and discussions to experts and representatives from APEC economies for use in risk management by stakeholders or persons in charge of genebanks to reduce risks related to all possible sources and to ensure that all GRs can be safely conserved and efficiently used for food and agriculture.

This Workshop consisted of plenary sessions, major symposia (including resource presentation and country reports), and field tours to visit scientific institutions, project areas, etc. The workshop provided an opportunity for participants to present, discuss, and share their experiences and technology on the following issues:

1. Information, knowledge, and practices regarding managements of GRs;
2. Particular problems, constraints, and risks of managing GRs;
3. Analysis of internal and external sources of risks and problems associated with managing GRs;
4. Mitigation of risks using existing technologies as well as human and organizational resources;
5. Development of new technologies for effectively and efficiently managing GRs;
6. Proposition of effective, secure, and practical management measures for GRs;
7. Good practices for the risk management of GRs *in situ* and/or on farm management; and
8. New developments and implementation of risk management for genebanks.

Opening session

1. Dr. Wu-Hsiung Chen, Minister of the COA, Chinese Taipei, officially opened the APEC-ATCWG Workshop and warmly welcomed everyone. He said that agriculture is crucial to the economies of the APEC members and with soaring food prices and socio-economic disruptions around the world, it is very important to ensure adequate food supplies. GRs are recognized worldwide as essential and have strong impacts on the global economy and social welfare. Thus, he said risk management is needed to reduce or prevent loss of genetic diversity caused by human and natural factors and ensure sustainable development in the food and agriculture sector. He called for the preservation of valuable GRs and recognized that in the realm of GR conservation, there are lots of experience and expertise to be shared among nations in the Asian-Pacific region. He felt honored and glad that Chinese Taipei was host to this important event. He believed that through sharing resources and exchanging expertise, this workshop would be of great help in formulating risk management of GRs and charting the future of GR management. Dr. Chen encouraged everyone to deliberate on core issues faced by great men and women managing GRs, and hoped that the field tour would enable all to know more about genebanks and the heritage of Chinese Taipei. He also wished all delegates and participants a rewarding experience in Taiwan.

2. In his Welcome Address, Dr. D.J. Liu, director general of TATI, stressed the importance of GRs to the global economy and to the sustainable development of human culture. He mentioned that in 1997, Chinese Taipei initiated the first workshop on GR subject, also held in TARI, and that five more workshops in different economies were held over the next 10 years. He observed that the mainstream activities in GR conservation are still going strong. He also cautioned that once extinct, a GR can no longer be recovered, and the negative effects of such loss on human beings would be tremendous. He said that minimizing risk to GR conservation could be realized if we could wisely maintain and manage GRs. Dr. Liu expressed his confidence in all the delegates and challenged that everyone “can do a little bit more by holding training courses in perpetuity and facilitating exchange” of materials, information, experiences, and expertise. Finally, he said that in addition to managing GRs, he encouraged everyone to become friends and have good memories during the workshop and throughout their stay in Taiwan.

3. The director general of the AVRDC-The World Vegetable Center, Dr. Dyno Keatinge, delivered the congratulatory remarks. He congratulated and thanked Chinese Taipei for

hosting this important workshop as well as the resource persons and the delegates for their attendance and participation. He pointed out that “we are entrusted with GRs not just for today but for many generations in the future.” He said that the great responsibility for taking care of these GRs for the sake of our grandchildren is the biggest risk. He urged that this responsibility be carried in perpetuity and called on everyone to maximize collaboration. Dr. Keatinge mentioned that Taiwan’s involvement in agricultural research goes back to 1895 and there are no problems and rice crisis in Taiwan. With crop diversification as an important dimension in agriculture, Taiwan’s agriculture has further developed. He said that other countries, including “the U.S. and the UK, which have been eroding their agriculture,” could learn from Taiwan’s multi-crop-based system of farming. He hailed “Taiwan as an excellent example to the world.”

Keynote speeches

Selected experts were invited to present keynote speeches in three sessions, with two papers per session. Discussions arising from the questions raised are summarized below.

Paper No. 1: Experiences from Establishing an International Seed Bank - Svalbard Global Seed Vault: Practical Management Measures – Dr. Jessica Kathle, NordGen

Experiences and practical measures from establishing an international seed bank were presented. The paper focused on the Svalbard Global Seed Vault, which is the most secure possible backup storage site for a global system of *ex situ* collections of crop diversity.

Two participants inquired about (1) variations in the black boxes, specifically for wild species; (2) the rules for regeneration, particularly what goes into the black boxes; and (3) whether any request for seed deposition has ever been rejected by Svalbard. The speaker clarified the policy on black boxes, as follows: (a) there are ongoing discussions as to the wild relatives that Svalbard would want to store; (b) regeneration depends on the original material, and Svalbard would advise the depositors because they have the responsibility for regeneration, and ownership of the seed remains with the depositor; and (c) so far, there has been no rejection, but for efficient storage, Svalbard does not want to keep mere copies or duplicates.

Two resource speakers from India and Canada, respectively, provided additional information, as follows:

- These black boxes are not very big, so they can store only limited amounts of seed. *(India)*
- NordGen provides information to depositors on the appropriate box to send and the box does not have to be hard plastic. Canada uses cardboard boxes. *(Canada)*

Paper No. 2: Preserving the Future of Vegetable Improvement – Dr. Dyno Keatinge, AVRDC

Dr. Keatinge discussed how the World Vegetable Center is preserving the future of vegetable improvement. The speaker pointed out that the World Vegetable Center has the world's largest collection of vegetables (56,000 accessions), has a broader crop portfolio, and is committed to the assembly and preservation of a genetically diverse germplasm collection. However, the collections are exposed to certain risks, foremost of which are earthquakes and flooding. It was pointed out that the risk of losing the vegetatively propagated species is higher than those propagated by seed. The participants were also reminded that it is important to know something about what we preserve, thus documentation and information sharing should be developed and maintained.

Some participants asked about (1) the difficulties in crop improvement, particularly breeding, compared to genetic resources improvement; and (2) the problem with activities with crops that do not set seed and the regeneration of F_1 seeds. The speaker pointed out that these issues should be discussed, because it is important to decide to just choose a few activities to focus on, e.g. seed system, production system, or others. In terms of effectiveness, rather than engaging in small activities, e.g. for crops that will not set seed, the work is transferred to another location or country, as in the case of onions which do not set seed at all in Thailand, so the work was transferred to Mali, West Africa.

Paper No.3: Management of Germplasm Collections and Enhancing Their Use by Mini Core and Molecular Approaches – Dr. Hari D. Upadhyaya, ICRISAT

Dr. Upadhyaya discussed the use of germplasm in crop improvement, the reasons for low use and the means to overcome them, the importance of having core and mini-core collections, as well as molecular characterization of such collections. He concluded that strategic research on core and mini-core collections can enhance the use of germplasm in breeding programs, both SSR and qualitative traits provide a fair measure of diversity, and molecular characterization of mini-cores and their convenient evaluation even for agronomic traits will help identify the agronomic desirability of germplasm lines.

To a participant's inquiry on the quality of core and mini-core collections, the speaker emphasized that (1) the quality of the entire collection depends on the quality of the parental line, and may depend on one important gene; (2) it is just by chance, but there is high probability, that rare alleles may be obtained in core and mini-core collections; and (3) that having a mini-core collection is an option.

Paper No. 4: Establish Taiwan Biodiversity Information Network and its Integration on Germplasm Databanks – Dr. Kwang-Tsao Shao, Academia Sinica

Dr. Shao mentioned about Taiwan's biodiversity information network (TaiBNET) and its integrated germplasm databank that boasts of 1434 species belonging to 189 families and 781 genera, with a total of 68,108 passport data, 27,581 records of characterization data, and 4002 images.

Participants asked about the software programs used, the problems encountered in the process of database integration, and the solutions used to address such problems. The speaker replied that TaiBNET uses internationally accepted software programs, and that the process of integration was facilitated by availability of adequate funding; the existence of a national action plan; the education of scientists through training sessions on database management; and frequent communication, meetings, and workshops with the scientists.

Paper No. 5: Enhanced Conservation and Management of Canadian Bioresources – Dr. Ken Richards, SRC-AAFC

This paper focused on the measures and practices that Canada has implemented to reduce the risk of losing its crop and livestock gene pools. Some practices mentioned for the seed storage vault were restricted access to and within the building; the use of entrance camera, motion sensors, and rocks as physical barrier; and installation of a fire suppressor system. For the cryogenic room, the following safety measures were cited: provisions for staff safety, oxygen sensors, camera, and emergency or "hot" buttons. The speaker also mentioned practical solutions and challenges for reducing genetic erosion. He pointed out that the GR program of Canada uses an integrated approach to conservation, and reduces risks through integrating basic GR functions and capacity building activities.

Paper No. 6: Risk Management in Microbial Genetic Resources in BCRC/FIRDI of Taiwan – Dr. Chii-Cherng Liao, FIRDI

Dr. Liao presented a comprehensive discussion of the microbial, cellular, and GRs of the Bioresource Collection and Resource Center (BCRC); the challenges and opportunities faced by microbial resource centers; the culture distribution of BCRC, and the risk management processes used to identify risks and the measures undertaken to mitigate such risks.

The speaker also mentioned that BCRC manages risks to its microbial resources through its facilities for access control, a biowarehouse management system, on-line control systems, and biosafety operation rooms at different levels. He further discussed the information risk identification process of BCRC to determine the source, vulnerability and threat. To address risks, the BCRC has a disaster discovery strategy, emergency response mechanism, and auditing processes.

Paper presentation by member economies

Three sessions were held for the presentation of 12 member economies, with three papers in the first session, two papers in the second, and five papers in the third session. Below is a summary of the discussions based on the questions and comments raised. In addition, some issues or concerns which were to be taken up in the concluding portion of the workshop were also identified.

Session 1

The following member economies were the presenters for this session: Canada (Dr. Ken Richards), Indonesia (Dr. Sutoro), and Japan (Dr. Makoto Kawase), with Dr. Workneh Ayalew of Papua New Guinea serving as moderator.

Dr. Richards elaborated on Canada's integrated repository system for plant, animals and microbial genetic resources; the current holdings, databases, and staff capability; and productivity in terms of publications, trainings, and manpower. On the other hand, Dr. Sutoro focused on the management of PGRs in Indonesia, particularly its *ex situ* conservation activities, core collections, and utilization of PGRs for commercial purposes. Indonesia recognized its need for more efficient methods of evaluating the germplasm; its characterization of the core must be representative of the entire collection and its data

collection from the core collection should be qualitative and quantitative, using cluster analysis. The presentation of Dr. Kawase discussed the present status and future prospects of the National Institute of Agrobiological Sciences (NIAS) project in Japan. The NIAS Genebank coordinates plant, animal, microorganism, and DNA genetic resources related to food and agriculture and a rice genome resource center. The NIAS project is implemented based on strong cooperation between Japan and its international partners, and its research component enhances conservation efforts with genetic resources. This genebank also serves as an international backup center for designated crops. A brochure featuring the role of the NIAS Genebank, its history and activities was also distributed.

Discussions:

- Canada is at the forefront of climate change and with methane as a cause of climate change, which are the real key sources of methane – animals or the plants? Among plants, are they the crucifers or the brassicas? At the moment, there is a need to determine basic information before there can be a change in plant GR management practices.
- Canada presently regenerates all of the materials in its genebank, has extensive breeding programs, and moves its breeder seeds through the chain, from foundation seeds to certified seeds.
- The GRIN system developed by the US is used by Canada; it is a very complicated system and the problems initially encountered were communicated with the US. Canada relied on the US Department of Agriculture (USDA) programmers, then trained its own staff on how to operate the system. In general, it took a while for Canada to converge its data. Dr. Richards is optimistic that the system will become simpler as new initiatives from the USDA are underway and moving to freer software with new upfront pages.
- In the future, DNA data can be matched with phenotypic data; at the moment there is no capability to do this.
- Japan's budget for genetic resources conservation is also shrinking, and that is becoming a problem. But it is able to deal with this because it functions as a network with different institutions – at the beginning it was all funded through the national government, but now semi-privatized. Budget from government has many restrictions. The different institutions, including laboratories and organizations, meet every year and agree on what project to implement.

- Recently, research institutions have been experiencing reorganization, and there is rapid change in personnel handling GR conservation. As a result, it is difficult to grasp the true state of GRs, and it has to be investigated and updated every year.
- Some caution was aired in handling cryopreservation for all genotypes and treatments.

Session 2

Presentations for this session were made by the following member economies: Korea (Dr. Jung-Hoon Kang) and Papua New Guinea (Dr. Ayalew), with Dr. Kawase of Japan as moderator.

Dr. Kang presented the status and progress of conservation and utilization of agricultural GRs in the Republic of Korea. Research highlights on the conservation and utilization of PGRs, information, and capacity building were also discussed. He also distributed a flyer featuring the opening of a world seed vault at Rural Development Administration (RDA) in Korea. On the other hand, Dr. Ayalew presented the status of management of plant, livestock, and aquaculture GRs in PNG. He also discussed the collaboration and networking activities, and the major constraints in the management of GRs.

Discussions:

- PNG is one of the world's richest and most-diverse nations and should be recognized as the second center of diversity for cassava.
- APEC should recognize the contribution of countries to diversity conservation.
- Baseline information/data from the various countries should be taken into consideration.
- Japan and Korea serve as duplicate repositories.
- Common problems should be further discussed and collaborative work on solving these problems could be identified.

Session 3

The third session featured 5 member economies, namely: Peru (Mr. Segundo Manuel Siguenas Saavedra), Philippines (Dr. Susan Sandra L. Ilao), Thailand (Ms Assanee Songserm), Vietnam (Ms.Tran Thi Tuyet Lan), and Chinese Taipei (Dr. Sheng-chung Huang), with Dr. Ilao as the moderator. The speakers from Peru, the Philippines, and Thailand

focused their presentations on the conservation and management of PGRs, while Vietnam and Chinese Taipei tackled the whole gamut of GRs – plant, livestock, fisheries, forestry, and microbes. All the country papers emphasized the need for strong national and international collaboration to ensure the success of GR conservation and risk management.

Mr. Manuel Sigüeñas talked about the management of the Peruvian biodiversity and the conservation of GRs for food and agriculture, its documentation system, and the capacity-building activities. Dr. Ilao discussed the status of PGRs for food and agriculture in the Philippines, and the capability building and R&D initiatives for PGRs, particularly those with interventions from her agency. Her paper also elaborated on the problems, constraints, and risk factors in PGR management. Ms. Songserm discussed the relevant organizations that are responsible for PGR conservation in Thailand and their activities. She presented the status of collections, the regeneration and utilization activities being conducted, and the potential risks that make PGR conservation and management difficult. Ms. Tran presented the status of the conservation of agriculture GRs in Vietnam, constraints, and future direction. Dr. Huang gave a comprehensive presentation of the conservation activities being done by the Plant Genetic Resources Center of the TARI, the Tree Seed Bank of the Taiwan Forestry Research Institute, the Taiwan Livestock Research Institute (TLRI), and the Freshwater Aquaculture Research Center of Taiwan Fisheries Research Institute. He pointed out that transgenic rice seeds carrying T-DNA are produced and conserved in TARI. He also discussed the country's efforts toward risk management, including natural risk mitigation strategies and capacity building.

Discussions:

- The presentations of the respective member economies in this session showed some unique features, yet there are a lot of commonalities that can serve as springboard for sharing and cooperation, as noted for further discussion in subsequent workshops.

  Uniqueness:

  The geographical characteristics of each country and inherent capacities of the member economies differ in terms of human and physical resources for implementing GR conservation. Thus, particularly for the PGRs, conservation and management of the crop/germplasm accessions differ in terms of type, number, and condition of facilities.

Commonalities:

1. Several institutions (research, academic, private, government, and non-government institutions) hold the germplasm *ex situ* collections for major or priority crops.
2. *In situ* conservation is usually done in natural protected areas.
3. Networking among institutions within the country and with international partners exists and enhances GR conservation.
4. Except perhaps for Chinese Taipei, the four other member economies (Peru, Philippines, Thailand, Vietnam) experience limited budget for infrastructure, equipment, human resource development, and capability building. The infrastructure for sustainable long-term conservation is needed.
5. Promoting public awareness is necessary.
6. Detailed evaluations are needed for the various collections.
7. Access to genetic resources information on the web needs to be developed (Peru) and enhanced. Certain limitations hamper the availability of the information, but development of the information systems and accessibility on the web are being worked out by the respective countries.
8. Capacity building needs to be sustained.

- As emphasized by Dr. Jessica Kathle in the first part of this workshop, no single country and no single genebank can possibly have a monopoly of plant, animal, fish, and forest genetic GRs. When the germplasm is lost, the traditional information about the material may also be lost. Hence, the importance of cooperation or collaboration was recognized, including workshops such as this, particularly in terms of identifying the risks to management of GRs. But the activities should not stop at identifying risks; there should be an effort to systematically determine the magnitude and frequency of risks, and identify the measures for mitigating such risks. As far as risk management is concerned, the paper presentations in this session showed that risks could be identified, but it seems there are no scientific studies on the assessing these risks, on prediction of the risks, or identifying mitigating measures.
- There was a lengthy discussion on the risk to genebanks regarding the management of transgenic crops/GMOs. Handling GMOs may be a problem in the future not only in terms of space but other matters, such as certification of the

GMO, provision for an isolated area for storage, a mechanism for handling the risk, and the need to rationalize the management of GMOs. This was pointed out as a major item for further discussion.

Issues and concerns for further discussion

This list summarizes the issues and concerns arising from the discussions during the presentation by member economies. These issues and concerns were considered in formulating action plans during the last part of this workshop.

1. Research at the level of genebank enhances management of GRs.
2. Germplasm is not sufficiently evaluated; detailed evaluation work is needed. More collaborative work can be carried out on this aspect.
3. There is a need for networking among institutions doing work on GRs at different management levels. Common problems should be identified which can be resolved by collaborative work.
4. Sustained capacity building (formal and non-formal) should be pursued.
5. Development, enhancement and/or standardization of information systems and making the information available on the web should be pursued; some may need assistance, e.g. training or funding.
6. Donations of GRs from the private sector seem substantial (as in the case of livestock semen) and may be pursued through collaboration.
7. The management of GMOs should be rationalized.

Concluding discussions (Formulation of action plans)

This summary lists the opinions and points raised by different participants towards the development of action plans.

1. Cooperation on capacity building in GR conservation and management
   - Rationalization of collections;
   - Minimize duplicates;
   - Target countries without backup collections;
   - Match experts with students doing technical work, e.g. molecular characterization;

- Match experts in one country with materials available in a particular country;
- Build the capacity of information systems (to determine what we have);
- Agree on what we put on websites (pictures, progress reports, etc.);
- Provide operational guidelines on sharing of materials;
- Provide risk management requirements on constructing genebank (*cross-over to #4*);
- Hold meetings among genebank managers and engineers. (*cross-over to #4*); and
- Know/consider what has been done in the past and look forward to "green technology". The structure appropriate many years ago might no longer be applicable today and in near future. (*cross-over to #4*)

2. Possibility of international collaboration on exchange of germplasm materials and information through national or government support of GRs
   - Enhance capacities of information systems (*cross-over to #1*);
   - Develop common databases for exchanging information;
     - There is fund at the USDA for enhancing the use of GRIN.
     - This may be difficult for countries with developed information systems or existing databases, but may be easier to adopt for countries just starting up their database system.
     - It is possible to provide some countries with the opportunity to go through the information systems and to initiate possible cooperation to persuade policymakers.
     - Some countries should be allowed to continue with their present system but be able to link with other systems.
     - Every country should develop its own information systems.
   - Invite experts for one week to meet together and discuss information systems; and
   - Establish or implement ABS system because some countries do not have it yet.
3. Development of new technologies for effective and efficient GR management
   - Develop molecular techniques for particular species;
   - Develop regeneration protocols (Some species have standard regeneration protocols);
   - Establish "Best practices" for conservation for specific crops;

- Manage risks;
- Use computer-aided techniques to decide on required materials;
- Promote cooperation and exchange of field research by researchers;
- Transfer technology and invent new technologies;
- Regarding *in situ* conservation in PNG, determine how many sites have obtained protection for GRs;
- Establish ways of determining if a population is worth conserving *in situ*;
- Emphasize the importance of public education/understanding of *in situ* conservation;
- Develop new techniques for indicator development;
- Expand cryopreservation to include clonal crop species; and
- Develop new technologies for more-secure backup system.

4. Mitigation of risks and recovery in case of natural calamities on genetic resources management
   - Refer to early chapters of *FAO World Report*;
   - Have secure duplicates remote from the country where the materials are at the present time;
   - Realize that genebanks are evolving, just as information is evolving;
   - Scientific study risks, by including socioeconomics experts and engineers;
   - Develop networks as a strategy to deal with risks;
   - Consider secondary duplicate of major important materials; and
   - Use the Svalbard Seed Vault as model of a strategy to mitigate risks.
5. Practical approaches in case of particular problems and constraints of risks on GR management
   - Remember that clients always want quality germplasm and complete information with regard to conservation and utilization of GRs;
   - As many countries are focused on research; sometimes genetic erosion occurs in a genebank. New technologies should be based on stock management; and
   - Will we move from *in situ* to *ex situ* conservation, or from *ex situ* to *in situ*?

PROGRAM

Monday, 13 October 2008

11:00-23:00 Arrival of participants

Tuesday, 14 October 2008

09:00-09:30 **Registration**

09:30-10:00 **Opening ceremony**

Opening remarks – Dr. Wu-Hsiung Chen, Minister, Council of Agriculture (COA), Chinese Taipei

Welcome address - Dr. D. J. Liu, Director General, Taiwan Agricultural Research Institute (TARI), COA, Chinese Taipei

Congratulatory remarks - Dr. Dyno Keatinge, Director General, AVRDC–The World Vegetable Center, Shanhua, Tainan, Taiwan

10:00-10:40 **Group photo and tea break**

Keynote Speeches (I)

Moderator: **Dr. Ken Richards**, Research Manager, Canadian Genetic Resources Program, Agriculture and Agri-Food Canada

10:40-11:20 Experiences from Establishing an International Seed Bank – Svalbard Global Seed Vault: Practical Management Measures. **Dr. Jessica Kathle**, Managing Director, Nordic Genetic Resource Center (NordGen), Sweden

11:20-12:00 Preserving the Future of Vegetable Improvement. **Dr. Dyno Keatinge**, Director General, AVRDC – The World Vegetable Center, Shanhua, Tainan, Taiwan

12:00-13:30 Lunch

Keynote Speeches (II)

Moderator: **Dr. Dyno Keatinge**, Director General, AVRDC - The World Vegetable Center, Shanhua, Tainan, Taiwan

13:30-14:10 Management of Germplasm Collections and Enhancing Their Use by Mini Core and Molecular Approaches. **Dr. Hari D Upadhyaya**, Principal Scientist of Genetic Resources, International Crops Research Institute for the Semi Arid Tropics (ICRISAT), Andhra Pradesh, India

14:10-14:50 Establish Taiwan Biodiversity Information Network and Its Integration on Germplasm Databanks. **Dr. Kwang-Tsao Shao,** Executive Director/Research Fellow, Biodiversity Research Center, Academia Sinica, Chinese Taipei

14:50-15:10 Tea break

Keynote Speeches (III)

Moderator**: Dr. Hari D Upadhyaya**, Principal Scientist of Genetic Resources, International Crops Research Institute for the Semi Arid Tropics (ICRISAT), Andhra Pradesh, India

15:10-15:50 Enhanced Conservation and Management of Canadian Bioresources. **Dr. Ken Richards**, Research Manager, Canadian Genetic Resources Program, Saskatoon Research Centre, Agriculture and Agri-Food Canada (AAFC)

15:50-16:30 Risk Management on Microbial Genetic Resources in BCRC/FIRDI of Taiwan. **Dr. Chii-Cherng Liao,** Deputy Director, Food Industry Research and Development Institute (FIRDI), Chinese Taipei

16:30-17:50 Highlighting the achievement of TARI. **Dr. D. J. Liu**, Director General, Taiwan Agricultural Research Institute (TARI)

Visit Plant Genetic Resources Center, TARI. **Dr. Sheng-Chung Huang**, Director, Division of Plant Germplasm, TARI

18:30-20:30 Welcome Reception hosted by **Dr. Wu-Hsiung Chen**, Minister, Council of Agriculture, Chinese Taipei

Wednesday, 15 October 2008

07:00-17:00 **Field trip**: Visit the National Animal Genebank, the Vegetable Genebank, and the Freshwater Fish Genebank

1. Livestock Research Institute, Council of Agriculture:
http://www.tlri.gov.tw/htm0/engnew.exe/?t=1

2. The World Vegetable Center: *http://www.avrdc.org/*

3. Freshwater Aquaculture Research Center, Fisheries Research Institute, Council of Agriculture: *http://www.tfrin.gov.tw/english/of.htm*

Thursday, 16 October 2008

Member Economy Presentation (I)

Moderator: **Dr. Workneh Ayalew,** Leader, Livestock Research Programme, Animal Genetic Resources and Improvement, National Agricultural Research Institute (NARI), Papua New Guinea

09:30-09:55 **Canada – Dr. Ken Richards**, Research Manager, Canadian Genetic Resources Program, Agriculture and Agri-Food Canada (AAFC)

09:55-10:20 **Indonesia – Dr. Sutoro**, Research Scientist, Indonesian Centre for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD)

10:20-10:45 **Japan – Dr. Makoto Kawase**, Director, Genebank of the National Institute of Agrobiological Sciences (NIAS)

10:45-11:10 Tea break

Member Economy Presentation (II)

Moderator: **Dr. Makoto Kawase**, Director, Genebank of the National Institute of Agrobiological Sciences (NIAS), Tsukuba, Japan

11:10-11:35 **Korea – Dr. Jung-Hoon Kang**, Head, Information Network, Genebank of the National Institute of Agricultural Biotechnology (NIAB), Rural Development Administration (RDA)

11:35-12:00 **Papua New Guinea – Dr. Workneh Ayalew,** Leader, Livestock Research Programme, Animal Genetic Resources and Improvement, National Agricultural Research Institute (NARI)

12:00-13:30 Lunch

Member Economy Presentation (III)

Moderator: **Dr. Susan Sandra L. Ilao**, Supervising Science Research Specialist and Head, Program Development & Resource Generation Unit, Crops Research Division, PCARRD, Philippines

13:30-13:55 **Peru – Mr. Segundo Manuel Sigüeñas Saavedra**, Specialist, Genetic Resources and Biotechnology, National Institute of Agricultural Innovation (INIA)

13:55-14:20 **Phillipines - Dr. Susan Sandra L. Ilao**, Supervising Science Research Specialist and Head, Program Development & Resource Generation Unit, Crops Research Division, PCARRD

14:20-14:45 **Thailand - Ms. Assanee Songserm**, Agricultural Scientist, Biotechnology Research and Development Office, Department of Agriculture (DOA)

14:45-15:10 **Vietnam - Ms. Tran Thi Tuyet Lan**, Senior Official, Department of Science, Ministry of Agriculture and Rural Development

15:10-15:35 **Chinese Taipei – Dr. Sheng-Chung Huang**, Director, Division of Plant Germplasm, TARI

15:35-16:00 Tea break

16:00-16:30 **Discussions and Conclusions**

Moderator: Dr. Ken Richards, Canada**;**

Dr. Makoto Kawase, Japan, and

Dr. D. J. Liu, Chinese Taipei

16:30-16:50 **Closing Ceremony**

17:00-18:00 Visit "**Taiwan Soil Museum**" at TARI

18:30-20:30 **Dinner** hosted by **Dr. D. J. Liu**, Director General, TARI, Chinese Taipei

Friday, 17 October 2008

07:00-17:00 **Field trip**: Visit the Food Industry Research and Development Institute, the Hsinchu Guansi Chin-Yong Recreational Farm, and the National Palace Museum

1. Food Industry Research and Development Institute (FIRDI): Genebank of Bioresources *http://www.firdi.org.tw/EngWeb/EngHPg.htm*

2. Hsinchu Guansi Chin-Yong Recreational Farm: *http://www.tomatohome.com.tw*

3. National Palace Museum: *http://www.npm.gov.tw/en/home.htm*

Saturday, 18 October 2008

Departure of participants

List of Participants －APEC/ATCWG Workshop

List of delegates

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Korea	Dr. Jung-Hoon Kang	Head of Information Network, RDA Genebank, National Institute of Agricultural Biotechnology (NIAB, RDA)	National Institute of Agricultural Biotechnology 225 Seodundong, Kwonseonku, Suwon 441-707 Rep. of Korea Tel: 82-31-299-1833 Fax: 82-31-294-6029 kjh3718@rda.go.kr
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Vietnam	Ms. Tran Thi Tuyet Lan	Senior Official Department of Science, Technology and Environment	Department of Science, Technology and Environment Ministry of Agriculture and Rural Development of Vietnam 2 Ngoc Ha, Hanoi, Vietnam Tel: 84-913030090 Fax: 84-4-8433637 lanttt.khcn@mard.gov.vn
Chinese Taipei	Dr. Sheng-Chung Huang	Director Division of Plant Germplasm, Taiwan Agricultural Research Institute (TARI)	Division Chief of Plant Germplasm, Taiwan Agricultural Research Institute, COA 189 Chung-Cheng Road, Wufeng, Taichung, 41301 Taiwan Tel: 886-4-23326670 Fax: 886-4-23331705 Mobile: 886-963-105082 schuang@wufeng.tari.gov.tw

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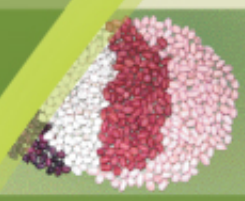

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